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<p>(21) International Application Number: PCT/US97/12955 (22) International Filing Date: 31 July 1997 (31.07.97)  (30) Priority Data: 08/708,541 5 September 1996 (05.09.96) US  (60) Parent Application or Grant (63) Related by Continuation US 08/708,541 (CIP) Filed on 5 September 1996 (05.09.96)  (71) Applicant (for all designated States except US): UNIVER- SITY OF MARYLAND - BIOTECHNOLOGY INSTI- TUTE [US/US]; Suite 500, 4321 Hartwick Road, College Park, MD 20740 (US).  (72) Inventors; and (75) Inventors/Applicants (for US only): VAKHARIA, Vikram, N. [US/US]; 11332 Booth Bay Way, Bowie, MD 20720 (US). MUNDT, Egbert [DE/DE]; Ring Strasse 12, D-17498 Rieusserorf (DE).</p>		<p>(74) Agents: KITTS, Monica, Chin et al.; Nikaido, Marmelstein, Murray &amp; Oram LLP, Suite 330, Metropolitan Square - "G" Street Lobby, 655 15th Street N.W., Washington, DC 20005-5701 (US).  (81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).  <b>Published</b> <i>With international search report.</i></p>
<p>(54) Title: A METHOD FOR GENERATING BIRNAVIRUS FROM SYNTHETIC RNA TRANSCRIPTS</p>		
<p>(57) Abstract</p> <p>A system for the generation of live Birnavirus such as infectious bursal disease virus (IBDV), a segmented double-stranded (ds)RNA virus of the <i>Birnaviridae</i> family, using synthetic transcripts derived from cloned DNA has been developed. Independent full-length cDNA clones were constructed which contained the entire coding and non-coding regions of RNA segments A and B of IBDV, respectively. Synthetic RNAs of both segments were produced by <i>in vitro</i> transcription of linearized plasmids with T7 RNA polymerase. Transfection of Vero cells with combined plus-sense transcripts of both segments generated infectious virus as early as 36 hours post-transfection. The development of a reverse genetics system for dsRNA viruses will greatly facilitate studies of the regulation of viral gene expression pathogenesis, and design of a new generation of live and inactivated vaccines.</p> <p style="text-align: center; font-size: 2em; font-weight: bold;">Best Available Copy</p>		

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## A METHOD FOR GENERATING BIRNAVIRUS FROM SYNTHETIC RNA TRANSCRIPTS

### Background of the Invention

Infectious bursal disease virus (IBDV), a member of the *Birnaviridae* family, is the causative agent of a highly immunosuppressive disease in young chickens (Kibenge, F.S.B., et al., *J. Gen. Virol.*, 69, 1757-1775 (1988)). Infectious bursal disease (IBD) or Gumboro disease is characterized by the destruction of lymphoid follicles in the bursa of Fabricius. In a fully susceptible chicken flock of 3-6 weeks of age the clinical disease causes severe immunosuppression, and is responsible for losses due to impaired growth, decreased feed efficiency, and death. Susceptible chickens less than 3 weeks old do not exhibit outward clinical signs of the disease but have a marked infection characterized by gross lesions of the bursa.

The virus associated with the symptoms of the disease is called infectious bursal disease virus (IBDV). IBDV is a pathogen of major economic importance to the nation and world's poultry industries. It causes severe immunodeficiency in young chickens by destruction of precursors of antibody-production B cells in the bursa of Fabricius. Immunosuppression causes increased susceptibility to other diseases, and interferes with effective vaccination against Newcastle disease, Marek's disease and infectious bronchitis disease viruses.

There are two known serotypes of IBDV. Serotype I viruses are pathogenic to chickens whereas serotype II viruses infect chickens and turkeys. The infection of turkeys is presently of unknown clinical significance.

IBDV belongs to a group of viruses called *Birnaviridae* which includes other bisegmented RNA viruses such as infectious pancreatic necrosis virus (fish), tellina virus and oyster virus (bivalve mollusks) and drosophila X virus (fruit fly). These viruses all contain high molecular weight (MW) double-stranded RNA genomes.

The capsid of the IBDV virion consists of several structural proteins. As many as nine structural proteins have been reported but there is evidence that some of these may have a precursor-product relationship (Kibenge,

F.S.B., et al., *J. Gen. Virol.*, 69, 1757-1775 (1988)). The designation and molecular weights of the viral proteins (VP) are as shown below.

5	Viral Protein	Molecular Weight
	VP1	90 kDa
	VP2	41 kDa
	VP3	32 kDa
	VP4	28 kDa
10	VP5	17 kDa

Two segments of double-stranded RNA were identified in the genome of IBDV. The IBDV genome consists of two segments of double-stranded (ds)RNA that vary between 2827 (segment B) to 3261 (segment A) nucleotide base pairs (Mundt, E. et al., *Virology*, 209, 10-18 (1995)). The larger segment A encodes a polyprotein which is cleaved by autoproteolysis to form mature viral proteins VP2, VP3 and VP4 (Hudson, P.J. et al., *Nucleic Acids Res.*, 14, 5001-5012 (1986)). VP2 and VP3 are the major structural proteins of the virion. VP2 is the major host-protective immunogen of IBDV, and contains the antigenic regions responsible for the induction of neutralizing antibodies (Azad, et al., *Virology*, 161, 145-152 (1987)). A second open reading frame (ORF), preceding and partially overlapping the polyprotein gene, encodes a protein (VP5) of unknown function that is present in IBDV-infected cells (Mundt, E., et al., *J. Gen. Virol.*, 76, 437-443, (1995)). The smaller segment B encodes VP1, a 90-kDa multifunctional protein with polymerase and capping enzyme activities (Spies, U., et al., *Virus Res.*, 8, 127-140 (1987); Spies, U., et al., *J. Gen. Virol.*, 71, 977-981 (1990)).

It has been demonstrated that the VP2 protein is the major host protective immunogen of IBDV, and that it contains the antigenic region responsible for the induction of neutralizing antibodies. The region containing the neutralization site has been shown to be highly conformation-dependent. The VP3 protein has been considered to be a group-specific antigen because

it is recognized by monoclonal antibodies directed against it from strains of both serotype I and II viruses. The VP4 protein appears to be a virus-coded protease that is involved in the processing of a precursor polyprotein of the VP2, VP3 and VP4 proteins.

5           Although the nucleotide sequences for genome segments A and B of various IBDV strains have been published, it was only recently that the complete 5'- and 3'-noncoding sequences of both segments were determined. The 5'-noncoding region of IBDV segments A and B contain a consensus sequence of 32 nucleotides, whereas the 3'-noncoding terminal sequences  
10 of both segments are unrelated, but conserved among IBDV strains of the same serotype (Mundt, E. et al., *Virology*, 209, 10-18 (1995)). These termini might contain sequences important in packaging and in the regulation of IBDV gene expression, as demonstrated for other dsRNA containing viruses such as mammalian and plant reoviruses, and rotaviruses (Anzola, et al., *Proc. Natl. Acad. Sci. USA*, 84, 8301-8305 (1987); Zou, S., et al., *Virology*, 186, 377-388 (1992); Gorziglia, M.I., et al., *Proc. Natl. Acad. Sci. USA*, 89, 5784-5788 (1992)).

          In recent years, a number of infectious animal RNA viruses have been generated from cloned cDNA using transcripts produced by DNA-dependent  
20 RNA polymerase (Boyer, J.C., et al., *Virology*, 198, 415-426 (1994)). For example poliovirus, a plus-stranded RNA virus; influenza virus, a segmented negative-stranded RNA virus; rabies virus, a non-segmented negative-stranded RNA virus; all were recovered from cloned cDNAs of their respective genomes (van der Werf, S., et al., *Proc. Natl. Acad. Sci. USA*, 83, 2330-2334  
25 (1986); Enami, M., et al., *Proc. Natl. Acad. Sci. USA*, 87, 3802-3805 (1990); Schnell, M.J., et al., *EMBO J.*, 13, 4195-4205 (1994)). For reovirus, it was shown that transfection of cells with a combination of SSRNA, dsRNA and *in vitro* translated reovirus products generated infectious reovirus when complemented with a helper virus from a different serotype (Roner, M.R., et al., *Virology*, 179, 845-852 (1990)). However, to date, there has been no  
30 report of a recovered infectious virus of segmented dsRNA genome from synthetic RNAs only.

### Summary of the Invention

This invention relates to the infectious bursal disease virus (IBDV) that is associated with Gumboro disease of young chickens. More particularly, this invention relates to a system for the generation of infectious bursal disease virus (IBDV) using synthetic transcripts derived from cloned cDNA. The present invention will facilitate studies of the regulation of viral gene expression, pathogenesis and design of a new generation of live and inactivated vaccines.

### Detailed Description of the Invention

In an effort to develop a reverse genetics system for IBDV, three independent full-length cDNA clones which contain segment A of serotype I strain D78 or serotype II strain 23/82 and segment B of the serotype I strain P2, respectively, were constructed. Synthetic RNAs of segments A and B were produced by *in vitro* transcription reaction on linearized plasmids with T7 RNA polymerase. Transcripts of these segments, either untreated or treated with DNase or RNase, were evaluated for the generation of infectious virus by transfection of Vero cells.

The present inventors have demonstrated that synthetic transcripts derived from cloned DNA corresponding to the entire genome of a segmented dsRNA animal virus can give rise to a replicating virus. The recovery of infectious virus after transfecting cells with synthetic plus-sense RNAs derived from cloned cDNA of a virus with a dsRNA genome (IBDV) completes the quest of generating reverse infectious systems for RNA viruses. A number of investigators have generated infectious animal RNA viruses from cloned cDNA (Boyer, J.C., et al., *Virology*, 198, 415-426 (1994)). Van der Werf et al. were first to generate poliovirus, a plus-stranded RNA virus, using synthetic RNA produced by T7 RNA polymerase on cloned cDNA template (van der Werf, S., et al., *Proc. Natl. Acad. Sci. USA*, 83, 2330-2334 (1986)). later, Enami et al. rescued influenza virus, a segmented negative-stranded RNA virus (Enami, M., et al., *Proc. Natl. Acad. Sci. USA*, 87, 3802-3805 (1990)); and Schnell et al. generated rabies virus, a non-segmented negative-stranded RNA virus, from cloned cDNAs of their respective genomes (Schnell, M.J., et

al., *EMBO J.*, 13, 4195-4205 (1994)). Roner et al. developed an infectious system for a segmented dsRNA reovirus by transfecting cells with a combination of synthetic ssRNA, dsRNA, *in vitro* translated reovirus products, and complemented with a helper virus of different serotype (Roner, M.R., et al., *Virology*, 179, 845-852 (1990)). The resulting virus was discriminated from the helper virus by plaque assay. However, in this system the use of a helper virus was necessary. In contrast, the presently described reverse genetics system of IBDV does not require a helper virus or other viral proteins. Transfection of cells with plus-sense RNAs of both segments was sufficient to generate infectious virus (IBDV). The fate of the additional one or four nucleotides, respectively, transcribed at the 3'-end of segment A was not determined. However, this did not prevent the replication of the viral dsRNA. Similar effects were observed for plus-stranded RNA viruses by different investigators (Boyer, J.C., et al., *Virology*, 198, 415-426 (1994)).

Transfection of plus-sense RNAs of both segments into the same cell was necessary for the successful recovery of IBDV. Transfected RNAs of both segments had to be translated by the cellular translation machinery. The polyprotein of segment A was presumably processed into VP2, VP3 and VP4 proteins which form the viral capsid. The translated protein VP1 of segment B probably acted as a RNA-dependent RNA polymerase and transcribed minus-strands from synthetic plus-strands of both segments, and the reaction products formed dsRNA. Recently, Dobos reported that *in vitro* transcription by the virion RNA-dependent RNA polymerase of infectious pancreatic necrosis virus (IPNV), a prototype virus of the *Bimaviridae* family, is primed by VP1 and then proceeds via an asymmetric, semiconservative, strand-displacement mechanism to synthesize only plus strands during replication of the viral genome (Dobos, P., *Virology*, 208, 10-25 (1995)). The present system shows that synthesis of minus-strands proceeds on the plus-strands. Whether the resulting transcribed minus-strand RNA serves as a template for the transcription of plus-strands or not remains the subject of further investigation.

To prove that the infectious IBDV contained in the supernatants of transfected cells was indeed derived from the synthetic transcripts, an artificial chimera was generated containing segment A of a serotype II strain and segment B of a serotype I strain. Sequence analysis verified this genome combination. The results also indicate that the terminal sequence motifs described by Mundt and Müller are probably responsible for replication, sorting and packaging of the viral genome (Mundt, E. et al., *Virology*, 209, 10-18 (1995)). Presence of serotype-specific terminal sequences obviously does not prevent proper replication of serotype II A segment by the action of the RNA-dependent RNA polymerase VP1 of the serotype I segment B. The ability to create recombinant viruses will greatly help in analyzing the precise function of serotype-specific and serotype-common terminal sequences.

The recovery of infectious IBDV demonstrates that only the plus-strand RNAs of both segments are sufficient to initiate replication of dsRNA. Thus, the results are in agreement with the general features of reovirus and rotavirus replication where the plus-strand RNAs serve as a template for the synthesis of progeny minus-strands to yield dsRNA (Schonberg, M., et al., *Proc. Natl. Acad. Sci. Patton, J.T., Virus Res.*, 6, 217-233 (1986); Chen, D., et al., *J. Virol.*, 68, 7030-7039 (1994)). However, the semiconservative, strand displacement mechanisms proposed by Spies et al. and Dobos could not be excluded (Spies, U., et al., *Virus Res.*, 8, 127-140 (1987); Dobos, P., *Virology*, 208, 10-25 (1995)). The development of a reverse genetics system for IBDV will greatly facilitate future studies of gene expression, pathogenesis, and help in the design of new generations of live and inactivated IBDV vaccines.

As used in the present application, the term "synthetic" as applied to nucleic acids indicates that it is a man made nucleic acid in contrast to a naturally occurring nucleic acid. The term implies no limitation as to the method of manufacture, which can be chemical or biological as long as the method of manufacture involves the intervention of man.

The term "cDNA" is intended to encompass any cDNA containing segments A and B and the 5' and 3' noncoding regions of segments A and B.



The term "infectious" as applied to viruses indicates that the virus has the ability to reproduce. The virus can be pathogenic or nonpathogenic and still be infectious.

5       The present invention provides a system for the generation of infectious bursal disease virus using synthetic RNA transcripts. This system can be used to study the regulation of viral gene expression, pathogenesis, and for the design of a new generation of live and inactivated IBDV vaccines.

10       The present invention provides a recombinant vector containing at least one copy of the cDNA according to the present invention. The recombinant vector may also comprise other necessary sequences such as expression control sequences, markers, amplifying genes, signal sequences, promoters, and the like, as is known in the art. Useful vectors for this purpose are plasmids, and viruses such as baculoviruses, herpes virus (HVT) and pox viruses, e.g., fowl pox virus, and the like.

15       Also provided herein is a host cell transformed with the recombinant vector of the present invention or a host cell transfected with the synthetic RNA of the present invention. The host cell may be a eukaryotic or a prokaryotic host cell. Suitable examples are *E. coli*, insect cell lines such as Sf-9, chicken embryo fibroblast (CEF) cells, chicken embryo kidney (CEK) cells, African green monkey Vero cells and the like.

20       Also part of this invention is an IBDV poultry vaccine comprising a poultry protecting amount of a recombinantly produced virus or portion of a virus, wherein the virus is inactivated or modified such that it is no longer virulent.

25       The virus can be inactivated by chemical or physical means. Chemical inactivation can be achieved by treating the virus with, for example, enzymes, formaldehyde,  $\beta$ -propiolactone, ethylene-imine or a derivative thereof, an organic solvent (e.g. halogenated hydrocarbon) and or a detergent. If necessary, the inactivating substance can be neutralized after the virus has been inactivated. Physical inactivation can be carried out by subjecting the viruses to radiation such as UV light, X-radiation, or  $\gamma$ -radiation.

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The virus can be attenuated by known methods including serial passage, deleting sequences of nucleic acids and site directed mutagenesis either before or after production of the infectious virus to produce a virus which retains sufficient antigenicity but which has reduced virulence.

5           Physiologically acceptable carriers for vaccination of poultry are known in the art and need not be further described herein. In addition to being physiologically acceptable to the poultry the carrier must not interfere with the immunological response elicited by the vaccine and/or with the expression of its polypeptide product.

10           Other additives, such as adjuvants and stabilizers, among others, may also be contained in the vaccine in amounts known in the art. Preferably, adjuvants such as aluminum hydroxide, aluminum phosphate, plant and animal oils, and the like, are administered with the vaccine in amounts sufficient to enhance the immune response to the IBDV. The amount of  
15           adjuvant added to the vaccine will vary depending on the nature of the adjuvant, generally ranging from about 0.1 to about 100 times the weight of the IBDV, preferably from about 1 to about 10 times the weight of the IBDV.

          The vaccine of the present invention may also contain various stabilizers. Any suitable stabilizer can be used including carbohydrates such  
20           as sorbitol, mannitol, starch, sucrose, dextrin, or glucose; proteins such as albumin or casein; and buffers such as alkaline metal phosphate and the like. A stabilizer is particularly advantageous when a dry vaccine preparation is prepared by lyophilization.

          The vaccine can be administered by any suitable known method of  
25           inoculating poultry including nasally, ophthalmically, by injection, in drinking water, in the feed, by exposure, and the like. Preferably, the vaccine is administered by mass administration techniques such as by placing the vaccine in drinking water or by spraying the animals' environment. When administered by injection, the vaccines are preferably administered  
30           parenterally. Parenteral administration as used herein means administration by intravenous, subcutaneous, intramuscular, or intraperitoneal injection.

The vaccine of the present invention is administered to poultry to prevent IBD anytime before or after hatching. Preferably, the vaccine is administered prior to the time of birth and after the animal is about 6 weeks of age. Poultry is defined to include but not be limited to chickens, roosters, hens, broilers, roasters, breeders, layers, turkeys and ducks.

The vaccine may be provided in a sterile container in unit form or in other amounts. It is preferably stored frozen, below  $-20^{\circ}\text{C}$ , and more preferably below  $-70^{\circ}\text{C}$ . It is thawed prior to use, and may be refrozen immediately thereafter. For administration to poultry the recombinantly produced virus may be suspended in a carrier in an amount of about  $10^4$  to  $10^7$  pfu/ml, and more preferably about  $10^5$  to  $10^6$  pfu/ml in a carrier such as a saline solution. The inactivated vaccine may contain the antigenic equivalent of  $10^4$  to  $10^7$  pfu/ml suspended in a carrier. Other carriers may also be utilized as is known in the art. Examples of pharmaceutically acceptable carriers are diluents and inert pharmaceutical carriers known in the art. Preferably, the carrier or diluent is one compatible with the administration of the vaccine by mass administration techniques. However, the carrier or diluent may also be compatible with other administration methods such as injection, eye drops, nose drops, and the like.

The invention also can be used to produce combination vaccines with the IBDV material. The IBDV material can be combined with antigen material of Newcastle Disease Virus Infectious Bronchitis virus, Reo virus, Adeno virus and/or the Marek virus.

The foregoing embodiments of the present invention are further described in the following Examples. However, the present invention is not limited by the Examples, and variations will be apparent to those skilled in the art without departing from the scope of the present invention.

#### Brief Description of the Drawings

Figure 1 is a schematic diagram of cDNA constructs used for synthesis of plus-sense ssRNAs of IBDV with T7 RNA polymerase. Construct pUC19FLAD78 contains the cDNA of segment A of IBDV strain D78 and the recombinant plasmid pUC18FLA23 contains the full-length cDNA of segment

A of IBDV strain 23/82. Segment A of IBDV encodes the polyprotein (VP2-VP4-VP3), and the recently identified VP5 protein. Plasmid pUC18FLBP2 contains the cDNA of segment B of strain P2 which encodes the RNA-dependent RNA polymerase (VP1). Virus specific sequences are underlined and the T7 promoter sequences are italicized. Restriction sites are shown in boldface and identified. The cleavage sites of the linearized plasmids are shown by vertical arrows and the transcription directions are marked by horizontal arrows.

Figure 2 shows an agarose gel analysis of the transcription reaction products that were used for transfection of Vero cells. Synthetic RNAs transcribed *in vitro* using T7 RNA polymerase and linearized plasmids pUC19FLAD78 (lanes 2, 4 and 6) containing the cDNA of segment A of IBDV strain D78, and pUC18FLBP2 (lanes 1, 3 and 5) containing the cDNA of segment B of strain P2, respectively. After transcription, the reaction mixtures were either treated with DNase (lanes 1 and 2), RNase (lanes 3 and 4) or left untreated (lanes 5 and 6). Two  $\mu$ l of the reaction products were analyzed on 1% agarose gel. Lambda DNA, digested with *Hind* III/*Eco*R I, was used as markers (lane M).

Figure 3 shows a comparison of nucleotide sequences of cloned RT-PCR fragments from segments A and B of the chimeric IBDV strain 23A/P2B (bold-typed) with known sequences of segments A and B of serotype II strain 23/82 and serotype I strain P2, respectively. Nucleotide identities are marked by a colon.

Figure 4 shows the DNA sequence of pUC18FLA23.

Figure 5 shows the DNA sequence of pUC19FLAD78.

Figure 6 shows the DNA sequence of pUC18FLBP2.

### EXAMPLES

**Viruses and Cells.** Two serotype I strains of IBDV, the attenuated P2 strain from Germany and the vaccine strain D78 (Intervet International), and one serotype II strain, the apathogenic 23/82 strain, were propagated in chicken embryo cells (CEC) and purified (Mundt, E. et al., *Virology*, 209, 10-18 (1995); Vakharia, V.N., et al., *Virus Res.*, 31, 265-273 (1994)). Vero cells

were grown in M199 medium supplemented with 5% fetal calf serum (FCS) and used for transfection experiments. Further propagation of the recovered virus and immunofluorescence studies were carried out in Vero cells (Mundt, E., et al., *J. Gen. Virol.*, 76, 437-443, (1995)). For plaque assay, monolayers of secondary CEC were prepared and used (Müller, H., et al., *Virus Res.*, 4, 297-309 (1986)).

**Construction of Full-Length cDNA Clones of IBDV genome.** Full-length cDNA clones of IBDV segments A and B were independently prepared. The cDNA clones containing the entire coding region of the RNA segment A of strain D78 were prepared using standard cloning procedures and methods (Vakharia, V.N., et al., *Virus Res.*, 31, 265-273 (1994)). By comparing the D78 terminal sequences with recently published terminal sequences of other IBDV strains (Mundt, E. et al., *Virology*, 209, 10-18 (1995)), it was observed that D78 cDNA clones lacked the conserved first 17 and last 10 nucleotides at the 5'- and 3'-ends, respectively. Therefore, to construct a full-length cDNA clone of segment A, two primer pairs (A5'-D78, A5-IPD78 and A3'-IPD78) were synthesized and used for PCR amplification (Table 1). The DNA segments were amplified according to the protocol of the supplier (New England Biolabs) using "Deep Vent Polymerase" (high fidelity thermophilic DNA polymerase). Amplified fragments were cloned into the *EcoR* I site of a pCRII vector (Invitrogen Corp.) to obtain plasmids pCRD78A5' and pCRD78A3', respectively. Each plasmid was digested with *EcoR* I and *Sal* I and the resultant fragments were ligated into *EcoR* I digested pUC19 to obtain plasmid pUC19FLAD78 (SEQ ID NOS:27 AND 29) which now contains a full-length cDNA copy of segment A encoding all the structural proteins (VP2, VP4 and VP3, SEQ ID NO:30) as well as the non-structural VP5 protein (SEQ ID NO:28) (Fig. 1).

Two primer pairs (A5'-23, A5IP23 and A3'-23, A3-IP23; see Table 1) were used for reverse transcription (RT) of viral genomic dsRNA of strain 23/82 using "SuperScript RT II" (RNA directed DNA polymerase with reduced RNase H activity, GIBCO/BRL). The RT reaction products were purified by phenol/chloroform extraction and ethanol precipitation. To obtain two cDNA

fragments bounded by primer pairs A5'-23, A5-IP23 and A3'-23, A3-IP23, respectively, RT reaction products were amplified by PCR using "Deep Vent polymerase". Both RT and PCR were carried out according to the supplier's protocol. Resulting PCR fragments were blunt-end ligated into *Sma* I cleaved pUC18 vector to obtain pUC23A5' and pUC23A3'. The 3'-end of segment A contained in plasmid pUC23A3' was ligated into the *Hind* III-*Bst* B I cleaved plasmid pUC23A5' to establish the full-length cDNA of segment A of strain 23/82. The resulting plasmid was termed pUC18FLA23 (SEQ ID NOS: 31 AND 33)(Fig. 1) and encodes structural proteins VP2, VP3 and VP4 (SEQ ID NO: 32) and non-structural protein VP5 (SEQ ID NO: 34)

To obtain cDNA clones of segment B of P2 strain, two primer pairs (B5'-P2, B5-IPP2 and B3'-P2, B3-IPP2) were designed according to the published sequences and used for RT-PCR amplification (see Table 1). Using genomic dsRNA as template, cDNA fragments were synthesized and amplified according to the supplier's protocol (Perkin-Elmer Cetus). Amplified fragments were blunt-end ligated into *Sma* I cleaved pBS vector (Stratagene) to obtain clones pBSP2B5' and pBSP2B3'. To construct a full-length clone of segment B, the 5'-end fragment of plasmid pBSP2B5' was first subcloned between *Eco*R I and *Pst* I sites of pUC18 vector to obtain pUCP2B5'. Then the 3'-end fragment of plasmid pBSP2B3' was inserted between the unique *Bgl* II and *Pst* I sites of plasmid pUCP2B5' to obtain a full-length plasmid pUC18FLBP2 (SEQ ID NO:25) which encodes the VP1 protein (SEQ ID NO: 26) (Fig. 1). Plasmids pUC18FLBP2, pUC18FLA23 and pUC19FLAD78 were completely sequenced by using the "Sequenase" DNA sequencing system (U.S. Biochem.), and the sequence data were analyzed using either "DNASIS" (Pharmacia) or "PC/Gene" (Intelligenetics) software. The integrity of the full-length constructs was tested by *in vitro* transcription and translation coupled reticulocyte lysate system using T7 RNA polymerase (Promega).

**Transcription and Transfection of Synthetic RNAs.** Plasmids pUC19FLAD78, pUC18FLA23 and pUC18FLBP2 were digested with *Bsr*G I, *Nsi* I and *Pst* I enzymes (see Fig. 1), respectively, and used as templates for *in vitro* transcription with T7 RNA polymerase (Promega). Briefly, restriction

enzyme cleavage assays were adjusted to 0.5% SDS and incubated with proteinase K (0.5 mg/ml) for 1 hour at 37°C. The linearized DNA templates (~3 µg) were recovered after ethanol precipitation, and were added separately to a transcription reaction mixture (50 µl) containing 40 mM Tris-HCl (pH 7.9), 10 mM NaCl, 6 mM MgCl<sub>2</sub>, 2 mM spermidine, 0.5 mM ATP, CTP and UTP each, 0.1 mM GTP, 0.25 mM cap analog [m<sup>7</sup>G(5') PPP(5') G], 120 units of "RNasin" (ribonuclease inhibitor), 150 units T7 RNA polymerase (Promega), and incubated at 37°C for 1 hour. Synthetic RNA transcripts were purified by phenol/chloroform extraction and ethanol precipitation. As controls, the transcription products were treated with either DNase or RNase (Promega) before the purification step.

Vero cells were grown to 80% confluence in 60 mm dishes and washed once with phosphate-buffered saline (PBS). Three ml of "OPTI-MEM I" (reduced serum medium containing HEPES buffer, sodium bicarbonate, hypoxanthine, thymidine, sodium pyruvate, L-glutamine, trace elements, growth factors and phenol red; from GIBCO/BRL) were added to the monolayers, and the cells were incubated at 37°C for 1 hour in a CO<sub>2</sub> incubator. Simultaneously, 0.15 ml of "OPTI-MEM I" was incubated with 1.25 µg of "Lipofectin" reagent (N-[1-(2,3-dioleyloxy)propyl]-N,N,N-trimethylammonium chloride and dioleoylphosphatidylethanolamine, GIBCO/BRL) for 45 min. in a polystyrene tube at room temperature. Synthetic RNA transcripts of both segments, resuspended in 0.15 ml of diethyl pyrocarbonate-treated water, were added to the OPTI-MEM-Lipofectin-mixture, mixed gently, and incubated on ice for 5 min. After removing the "OPTI-MEM" from the monolayers in 60 mm dishes and replacing with fresh 1.5 ml of "OPTI-MEM", the nucleic acid containing mixture was added drop-wise to the Vero cells and swirled gently. After 2 hours of incubation at 37°C, the mixture was replaced with M199 medium [CaCl<sub>2</sub> (anhydrous), Fe(NO<sub>3</sub>)<sub>3</sub> 9H<sub>2</sub>O, KCl, MgSO<sub>4</sub> (anhydrous), NaCl, NaH<sub>2</sub>PO<sub>4</sub>·H<sub>2</sub>O, NaHCO<sub>3</sub>, L-Alanine, L-Arginine HCl, L-Aspartic acid, L-Cysteine HCl H<sub>2</sub>O, L-Cysteine 2HCl, L-Glutamic acid, L-Glutamine, Glycine, L-Histidine HCl H<sub>2</sub>O, L-Hydroxyproline, L-Isoleucine, L-Leucine, L-Lysine HCl, L-Methionine, L-Phenylalanine, L-

Proline, L-Serine, L-Threonine, L-Tryptophan, L-Tyrosine 2Na 2H<sub>2</sub>O, L-Valine, Alpha tocopherol PO<sub>4</sub> Na<sub>2</sub>, Ascorbic Acid, Biotin, Calciferol, D-Calcium pantothenate, Choline chloride, Folic acid, I-Inositol, Menandione NaHSO<sub>3</sub> 3H<sub>2</sub>O, Niacin, Nicotinamide, Para-aminobenzoic acid, Pyridoxine HCl, 5 Riboflavin, Thiamine HCl, Vitamin A Acetate, Adenine SO<sub>4</sub>, Adenylic Acid, ATP, Na<sub>2</sub>, Cholesterol, 2-Deoxy-D-Ribose, D-Glucose, Glutathione, Guanine HCl, Hypoxanthine Na, Phenol Red Na, Ribose, Sodium Acetate (anhydrous), Thymine, Tween 80, Uracil, and Xanthine Na; from Mediatech, Inc.] containing 5% FCS (without rinsing cells) and the cells were further incubated at 37°C 10 for desired time intervals.

**Identification of Generated IBDV.** CEC were infected with filtered (0.2 µm) supernatant from Vero cells transfected with transcripts of pUC18FLA23 and pUC18FLP2B. 16 hours post-infection, the whole cell nucleic acids were isolated (Mundt, E. et al., *Virology*, 209, 10-18 (1995)). 15 Primers were designed according to the published sequences and RT-PCR fragments were amplified, cloned and sequenced (Mundt, E. et al., *Virology*, 209, 10-18 (1995)). Sequence data were analyzed by using "DNASIS" software.

20 **Immunofluorescence.** Vero cells, grown on cover slips to 80% confluence, were infected with the supernatants derived from transfected Vero cells (after freeze-thawing) and incubated at 37°C for two days. The cells were then washed, fixed with acetone and treated with polyclonal rabbit anti-IBDV serum. After washing, the cells were treated with fluorescein 25 labeled goat-anti-rabbit antibody (Kirkegaard & Perry Lab.) and examined by fluorescence microscope.

**Plaque Assay.** Monolayers of secondary CEC, grown in 60 mm dishes, were inoculated with the supernatants derived from transfected Vero cells. After 1 hour of infection, the cells were washed once with PBS and 30 overlaid with 0.8% Agar noble (Difco) containing 10% tryptose phosphate broth, 2% FCS, 0.112% NaHCO<sub>3</sub>, 10<sup>3</sup> units penicillin, 10<sup>3</sup> µg/ml streptomycin, 0.25 µg/ml fungizone, 0.005% neutral red, 0.0015% phenol red. The cells



were incubated at 37°C for 2 to 3 days until plaques could be observed and counted (Müller, H., et al., *Virus Res.*, 4, 297-309 (1986)).

**Construction of Full-Length cDNA clones of IBDV Genome.** To develop a reverse genetics system for the dsRNA virus IBDV, two independent cDNA clones were constructed that contain segment A of strain D78 and segment B of strain P2 (Fig. 1). Each plasmid encoded either the precursor of structural proteins (VP2, VP4, VP3) and VP5 or only VP1 protein (RNA-dependent RNA polymerase). Plasmid pUC18FLBP2 upon digestion with *Pst* I and transcription *in vitro* by T7 RNA polymerase, would yield RNA containing the correct 5'- and 3'-ends. Whereas, upon digestion with *Bsr*G I and transcription, plasmid pUC19FLAD78 would yield RNA containing the correct 5'-end but with additional four nucleotides at the 3'end. Coupled transcription and translation of the above plasmids in a rabbit reticulocyte system yielded protein products that were correctly processed and comigrated with the marker IBDV proteins after fractionating on SDS-polyacrylamide gel and autoradiography (data not shown).

**Transcription, Transfection and Generation of Infectious Virus.** Plus-sense transcripts of IBDV segment A and B were synthesized separately *in vitro* with T7 RNA polymerase using linearized full-length cDNA plasmids as templates (see Fig. 2). Although two species of RNA transcripts were observed for segment B on a neutral gel (lanes 1 and 5), fractionation of these samples on a denaturing gel yielded only one transcript-specific band (data not shown). In order to show that plus-sense RNA transcripts of both segments are needed for the generation of infectious virus, the transcription mixtures were incubated with different nucleases, as shown in Fig. 2. Synthetic RNAs recovered after treating the transcription products with DNase (lanes 1+2), RNase (lanes 3+4) or without treatment (lanes 5+6), were used for the transfection of Vero cells. As mock control, Lipofectin alone was used. Five days post-transfection, cytopathic effect (CPE) was only visible in Vero cells transfected with combined transcripts of untreated or DNase-treated transcription products, but not with RNase-treated transcription mixtures or

mock-transfected control. In addition, no CPE was detected when Vero cells were transfected with RNA of only segment A or B (data not shown). These results demonstrate that replication of IBDV ensued after transfection of Vero cells with plus-sense ssRNAs of both segments of IBDV. To verify that the agent causing the CPE in Vero cells was indeed IBDV, transfected Vero cells were freeze-thawed, and supernatants were clarified by centrifugation, and used to infect CEC or Vero cells. CEC infected with the supernatants derived from Vero transfected cells of untreated or DNase-treated transcription mixtures produced CPE in one day post-inoculation (Table 2). However, no CPE could be detected even after five days in CEC, with the supernatants from transfected Vero cells of RNase-treated transcription mixtures, untreated segment A or B transcription mixtures and mock-transfected Vero cells. Similarly, when Vero cells on cover slips were infected with the same supernatants as described above and examined by immunofluorescence staining after 2 days, only supernatants derived from transfected Vero cells of untreated or DNase-treated transcription mixtures gave positive immunofluorescence signal (Table 2).

**Recovery of Transfectant Virus.** To determine the time point for the recovery of infectious virus, Vero cells were transfected with combined RNA transcripts of segments A and B. At 4, 8, 16, 24, 36 and 48 hours post-transfection, the supernatants were examined for the presence of transfectant virus by infectivity and plaque assays, as shown in Table 3. Our results indicate that the virus could be recovered as early as 36 hours after transfection. Virus titer was  $2.3 \times 10^2$  pfu/ml which appear to drop for samples obtained later than 48 hours after transfection.

**Generation of a Chimeric Virus.** To prove that plus-sense ssRNA of both segments of IBDV are sufficient for recovery of infectious virus, a chimeric IBDV was generated. Plasmid pUC18FLA23 containing a full-length sequence of segment A of serotype II strain was linearized by *Nsi* I digestion and ssRNA was synthesized *in vitro* using T7 RNA polymerase. The ssRNA transcript specifies the correct 5'-end but contains one additional residue at the 3'-end (Fig. 1). Vero cells were transfected with ssRNA of segment A of

serotype II strain 23/82 and ssRNA of segment B of serotype I strain P2. Five days after transfection when CPE was evident, the supernatant was clarified (after freeze-thawing) and used to infect CEC. After a second passage in CEC, genomic RNA of the virus was analyzed by RT-PCR and sequencing of the PCR products. Primers for segment A were designed to specifically amplify only segment A sequences derived from the serotype II strain. Primer for segment B bound to sequences of both serotypes. The amplified fragments were cloned and sequenced. The obtained segment A sequences showed a perfect match with known segment A sequences of serotype II strain 23/82, whereas segment B sequence exhibited complete homology to published segment B sequences of serotype I strain P2 (Fig. 3).

Table 1. Oligonucleotides Used for the Construction of Full Length cDNA Clones of IBDV Genomic Segments A and B.

Nucleotide Sequence	Orientation	Name	Nucleotide Number
TAATACGACTCACTATAGGATACGATCGGTCIGACCCCGGGGAGTCA	(+)	A5'-D78	1-31
AGAGAAATTC TAATACGACTCACTATAGGATACGATCGGTCIGAC	(+)	A5'-23	1-48
TGTACAGGGGACCCGCGAACGGATCCAAAT	(-)	A3'-D78	3237-3261
CGGCGAATTCATGCATAGGGGACCCCGCGAACGGATC	(-)	A3'-23	3242-3261
CGTCGACTACGGGATTCCTGG	(-)	A5-IPD78	1711-1730
CAGAGGCAGTACTCCGTCIG	(-)	A5-IP23	1971-1990
AGTCGACGGGATCTTGCTT	(+)	A3-IPD78	1723-1742
GAAGGTGTGCGAGAGGAC	(+)	A3-IP23	1883-1900
AGAGAAATTC TAATACGACTCACTATAGGATACGATGGGTCIGAC	(+)	B5'-P2	1-18
CGATCTGCTGCAGGGGCGCCCGCAGGCGAAGG	(-)	B3'-P2	2807-2827
CTTGAGACTCTTGTTCTCTACTCC	(-)	B5-IPP2	1915-1938
ATACAGCAAAGATCTCGGG	(+)	B3-IPP2	1839-1857

Composition and location of the oligonucleotide primers used for cloning. T7 promoter sequences are marked with italic types, the virus specific sequences are underlined, and the restriction sites marked in boldface. Orientation of the virus specific sequence of the primer is shown for sense (+) and antisense (-). The positions where the primers bind (nucleotide number) are according to the published sequences of P2 strain (2).

**Table 2.** Generation of Infections IBDV From Synthetic RNAs of Segment A and B.

Material Transfected	CPE	Immunofluorescence
ssRNA A+B, DNase-treated	+	+
ssRNA A+B, RNase-treated	-	-
ssRNA A+B, untreated	+	+
ssRNA A, untreated	-	-
ssRNA B, untreated	-	-
Lipofectin only	-	-

Vero cells were transfected with synthetic RNAs of segment A and B derived from transcription reactions that were either untreated or treated with DNase or RNase. After 5 days, the supernatants were collected, clarified by centrifugation, and analyzed for the presence of virus. The infectivity of the recovered virus was determined in CEC by the appearance of cytopathic effect (CPE) 1-2 days post-inoculation. The specificity of the recovered virus was determined by immunofluorescence staining of infected Vero cells with rabbit anti-IBDV serum.

**Table 3. Recovery of Virus at Various Times Post-Transfection.**

Time in hours post-transfection	CPE	Immunofluorescence	pfu/ml
4	-	-	0
8	-	-	0
16	-	-	0
24	-	-	0
36	+	+	$2.3 \times 10^2$
48	+	+	$6.0 \times 10^1$

Vero cells were transfected with synthetic RNAs of segment A and B as described. The infectivity and specificity of the recovered virus was detected by CPE in CEC and immunofluorescence staining in Vero cells, respectively. Monolayers of secondary CEC were used for plaque assay after inoculating the cells with the supernatants derived from transfected Vero cells. Approximate titer of the virus was calculated as plaque forming units per ml (pfu/ml).

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: VAKHARIA, Vikram N.  
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(ii) TITLE OF INVENTION: A METHOD FOR GENERATING BIRNAVIRUS  
FROM SYNTHETIC RNA TRANSCRIPTS

(iii) NUMBER OF SEQUENCES: 34

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(F) ZIP: 20005-5701

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US

(B) FILING DATE:

(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: P8172-6002

## (ix) TELECOMMUNICATION INFORMATION:

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## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: cDNA

22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCGGCT TTAATACGAC TCACTATAGG ATACGATCGG TCTGAC

46

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AATTGGATCC GTTCGCGGGT CCCCTGTACA AAGCCGAATT C

41

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGGCGAATTC ATGCATAGGG GACCCGCGAA CGGATC

36

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTCAGACCGA TCGTATCCTA TAGTGAGTCG TATTAGAATT CTCT

44

(2) INFORMATION FOR SEQ ID NO:5:



- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTGCATGCCT GCAGGGGGCC CCCGCAGGCG AAG

33

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCGTATCCTA TAGTGAGTCG TATTAGAATT C

31

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 120 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGAAGCCTGA GTGAGTTGAC TGACTACAGC TACAACGGGC TGATGTCAGC CACTGCCAAC 60

ATCAACGACA AGATCGGGAA CGTTCTAGTT GGAGAAGGGG TGACTGTTCT CAGTCTACCG 120

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 120 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGAAGCCTGA GTGAGTTGAC TGACTACAGC TACAACGGGC TGATGTCAGC CACTGCGAAC 60

ATCAACGACA AGATCGGGAA CGTTCTAGTT GGAGAAGGGG TGACTGTTCT CAGTCTACC 119

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGAAGCCTGA GTGAACTGAC AGATGTTAGC TACAATGGGT TGATGTCTGC AACAGCCAAC 60

ATCAACGACA AAATTGGGAA CGTCCTAGTA GGGGAAGGGG TCACCGTCCT CAGCTTACCC 120

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTTTCAATAG TCCACAGGCG CGAACGAAGA TCTCAGCAGC GTTCGGCATA AAGCCTACTG 60

CTGGACAAGA CGTGGAAGAA CTCTTGATCC CCAAAGTCTG GGTGCCACCT GAGGATCCGC 120

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTTTCAACAG TCCACAGGCG CGAAGCACGA TCTCAGCAGC GTTCGGCATA AAGCCTACTG 60  
CTGGACAAGA CGTGGAAGAA CTCTTGATCC CTAAAGTTTG GGTGCCACCT GAGGATCCGC 120

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTTCAACAG TCCACAGGCG CGAAGCACGA TCTCAGCAGC GTTCGGCATA AAGCCTACTG 60  
CTGGACAAGA CGTGGAAGAA CTCTTGATCC CTAAAGTTTG GGTGCCACCT GAGGATCCGC 120

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TAATACGACT CACTATAGGA TACGATCGGT CTGACCCCGG GGGAGTCA 48

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGAGAATTCT AATACGACTC ACTATAGGAT ACGATCGGTC TGAC

44

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TGTACAGGGG ACCCGCGAAC GGATCCAATT

30

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGGCGAATTC ATGCATAGGG GACCCGCGAA CGGATC

36

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGTCGACTAC GGGATTCTGG

20

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

27

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CAGAGGCAGT ACTCCGTCTG

20

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGTCGACGGG ATTCTTGCTT

20

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GAAGGTGTGC GAGAGGAC

18

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 44 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AGAGAATTCT AATACGACTC ACTATAGGAT ACGATGGGTC TGAC

44

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGATCTGCTG CAGGGGGCCC CCGCAGGCGA AGG

33

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CTTGAGACTC TTGTTCTCTA CTCC

24

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATACAGCAAA GATCTCGGG

19

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2827 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 112..2745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGATACGATG GGTCTGACCC TCTGGGAGTC ACGAATTAAC GTGGCTACTA GGGGCGATAC	60
CCGCCGCTGG CCGCCACGTT AGTGGCTCCT CTTCTTGATG ATTCTGCCAC C ATG AGT	117
Met Ser	1
GAC ATT TTC AAC AGT CCA CAG GCG CGA AGC ACG ATC TCA GCA GCG TTC	165
Asp Ile Phe Asn Ser Pro Gln Ala Arg Ser Thr Ile Ser Ala Ala Phe	5 10 15
GGC ATA AAG CCT ACT GCT GGA CAA GAC GTG GAA GAA CTC TTG ATC CCT	213
Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu Ile Pro	20 25 30
AAA GTT TGG GTG CCA CCT GAG GAT CCG CTT GCC AGC CCT AGT CGA CTG	261
Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser Arg Leu	35 40 45 50
GCA AAG TTC CTC AGA GAG AAC GGC TAC AAA GTT TTG CAG CCA CGG TCT	309
Ala Lys Phe Leu Arg Glu Asn Gly Tyr Lys Val Leu Gln Pro Arg Ser	55 60 65
CTG CCC GAG AAT GAG GAG TAT GAG ACC GAC CAA ATA CTC CCA GAC TTA	357
Leu Pro Glu Asn Glu Glu Tyr Glu Thr Asp Gln Ile Leu Pro Asp Leu	70 75 80
GCA TGG ATG CGA CAG ATA GAA GGG GCT GTT TTA AAA CCC ACT CTA TCT	405
Ala Trp Met Arg Gln Ile Glu Gly Ala Val Leu Lys Pro Thr Leu Ser	85 90 95
CTC CCT ATT GGA GAT CAG GAG TAC TTC CCA AAG TAC TAC CCA ACA CAT	453
Leu Pro Ile Gly Asp Gln Glu Tyr Phe Pro Lys Tyr Tyr Pro Thr His	100 105 110
CGC CCT AGC AAG GAG AAG CCC AAT GCG TAC CCG CCA GAC ATC GCA CTA	501
Arg Pro Ser Lys Glu Lys Pro Asn Ala Tyr Pro Pro Asp Ile Ala Leu	115 120 125 130

CTC	AAG	CAG	ATG	ATT	TAC	CTG	TTT	CTC	CAG	GTT	CCA	GAG	GCC	AAC	GAG	549
Leu	Lys	Gln	Met	Ile	Tyr	Leu	Phe	Leu	Gln	Val	Pro	Glu	Ala	Asn	Glu	
				135					140						145	
GGC	CTA	AAG	GAT	GAA	GTA	ACC	CTC	TTG	ACC	CAA	AAC	ATA	AGG	GAC	AAG	597
Gly	Leu	Lys	Asp	Glu	Val	Thr	Leu	Leu	Thr	Gln	Asn	Ile	Arg	Asp	Lys	
			150					155						160		
GCC	TAT	GGA	AGT	GGG	ACC	TAC	ATG	GGA	CAA	GCA	AAT	CGA	CTT	GTG	GCC	645
Ala	Tyr	Gly	Ser	Gly	Thr	Tyr	Met	Gly	Gln	Ala	Asn	Arg	Leu	Val	Ala	
		165					170					175				
ATG	AAG	GAG	GTC	GCC	ACT	GGA	AGA	AAC	CCA	AAC	AAG	GAT	CCT	CTA	AAG	693
Met	Lys	Glu	Val	Ala	Thr	Gly	Arg	Asn	Pro	Asn	Lys	Asp	Pro	Leu	Lys	
	180					185					190					
CTT	GGG	TAC	ACT	TTT	GAG	AGC	ATC	GCG	CAG	CTA	CTT	GAC	ATC	ACA	CTA	741
Leu	Gly	Tyr	Thr	Phe	Glu	Ser	Ile	Ala	Gln	Leu	Leu	Asp	Ile	Thr	Leu	
195					200					205					210	
CCG	GTA	GGC	CCA	CCC	GGT	GAG	GAT	GAC	AAG	CCC	TGG	GTG	CCA	CTC	ACA	789
Pro	Val	Gly	Pro	Pro	Gly	Glu	Asp	Asp	Lys	Pro	Trp	Val	Pro	Leu	Thr	
				215					220					225		
AGA	GTG	CCG	TCA	CGG	ATG	TTG	GTG	CTG	ACG	GGA	GAC	GTA	GAT	GGC	GAC	837
Arg	Val	Pro	Ser	Arg	Met	Leu	Val	Leu	Thr	Gly	Asp	Val	Asp	Gly	Asp	
			230					235					240			
TTT	GAG	GTT	GAA	GAT	TAC	CTT	CCC	AAA	ATC	AAC	CTC	AAG	TCA	TCA	AGT	885
Phe	Glu	Val	Glu	Asp	Tyr	Leu	Pro	Lys	Ile	Asn	Leu	Lys	Ser	Ser	Ser	
	245						250					255				
GGA	CTA	CCA	TAT	GTA	GGT	CGC	ACC	AAA	GGA	GAG	ACA	ATT	GGC	GAG	ATG	933
Gly	Leu	Pro	Tyr	Val	Gly	Arg	Thr	Lys	Gly	Glu	Thr	Ile	Gly	Glu	Met	
	260					265					270					
ATA	GCT	ATC	TCA	AAC	CAG	TTT	CTC	AGA	GAG	CTA	TCA	ACA	CTG	TTG	AAG	981
Ile	Ala	Ile	Ser	Asn	Gln	Phe	Leu	Arg	Glu	Leu	Ser	Thr	Leu	Leu	Lys	
275					280					285					290	
CAA	GGT	GCA	GGG	ACA	AAG	GGG	TCA	AAC	AAG	AAG	AAG	CTA	CTC	AGC	ATG	1029
Gln	Gly	Ala	Gly	Thr	Lys	Gly	Ser	Asn	Lys	Lys	Lys	Leu	Leu	Ser	Met	
				295				300						305		
TTA	AGT	GAC	TAT	TGG	TAC	TTA	TCA	TGC	GGG	CTT	TTG	TTT	CCA	AAG	GCT	1077
Leu	Ser	Asp	Tyr	Trp	Tyr	Leu	Ser	Cys	Gly	Leu	Leu	Phe	Pro	Lys	Ala	
			310					315					320			
GAA	AGG	TAC	GAC	AAA	AGT	ACA	TGG	CTC	ACC	AAG	ACC	CGG	AAC	ATA	TGG	1125
Glu	Arg	Tyr	Asp	Lys	Ser	Thr	Trp	Leu	Thr	Lys	Thr	Arg	Asn	Ile	Trp	
		325					330					335				



TCA	GCT	CCA	TCC	CCA	ACA	CAC	CTC	ATG	ATC	TCT	ATG	ATC	ACC	TGG	CCC	1173
Ser	Ala	Pro	Ser	Pro	Thr	His	Leu	Met	Ile	Ser	Met	Ile	Thr	Trp	Pro	
340						345				350						
GTG	ATG	TCC	AAC	AGC	CCA	AAT	AAC	GTG	TTG	AAC	ATT	GAA	GGG	TGT	CCA	1221
Val	Met	Ser	Asn	Ser	Pro	Asn	Asn	Val	Leu	Asn	Ile	Glu	Gly	Cys	Pro	
355					360			365							370	
TCA	CTC	TAC	AAA	TTC	AAC	CCG	TTC	AGA	GGA	GGG	TTG	AAC	AGG	ATC	GTC	1269
Ser	Leu	Tyr	Lys	Phe	Asn	Pro	Phe	Arg	Gly	Gly	Leu	Asn	Arg	Ile	Val	
				375					380					385		
GAG	TGG	ATA	TTG	GCC	CCG	GAA	GAA	CCC	AAG	GCT	CTT	GTA	TAT	GCG	GAC	1317
Glu	Trp	Ile	Leu	Ala	Pro	Glu	Glu	Pro	Lys	Ala	Leu	Val	Tyr	Ala	Asp	
			390					395						400		
AAC	ATA	TAC	ATT	GTC	CAC	TCA	AAC	ACG	TGG	TAC	TCA	ATT	GAC	CTA	GAG	1365
Asn	Ile	Tyr	Ile	Val	His	Ser	Asn	Thr	Trp	Tyr	Ser	Ile	Asp	Leu	Glu	
		405					410					415				
AAG	GGT	GAG	GCA	AAC	TGC	ACT	CGC	CAA	CAC	ATG	CAA	GCC	GCA	ATG	TAC	1413
Lys	Gly	Glu	Ala	Asn	Cys	Thr	Arg	Gln	His	Met	Gln	Ala	Ala	Met	Tyr	
	420					425					430					
TAC	ATA	CTC	ACC	AGA	GGG	TGG	TCA	GAC	AAC	GGC	GAC	CCA	ATG	TTC	AAT	1461
Tyr	Ile	Leu	Thr	Arg	Gly	Trp	Ser	Asp	Asn	Gly	Asp	Pro	Met	Phe	Asn	
435					440					445					450	
CAA	ACA	TGG	GCC	ACC	TTT	GCC	ATG	AAC	ATT	GCC	CCT	GCT	CTA	GTG	GTG	1509
Gln	Thr	Trp	Ala	Thr	Phe	Ala	Met	Asn	Ile	Ala	Pro	Ala	Leu	Val	Val	
				455					460					465		
GAC	TCA	TCG	TGC	CTG	ATA	ATG	AAC	CTG	CAA	ATT	AAG	ACC	TAT	GGT	CAA	1557
Asp	Ser	Ser	Cys	Leu	Ile	Met	Asn	Leu	Gln	Ile	Lys	Thr	Tyr	Gly	Gln	
			470					475						480		
GGC	AGC	GGG	AAT	GCA	GCC	ACG	TTC	ATC	AAC	AAC	CAC	CTC	TTG	AGC	ACA	1605
Gly	Ser	Gly	Asn	Ala	Ala	Thr	Phe	Ile	Asn	Asn	His	Leu	Leu	Ser	Thr	
		485					490					495				
CTA	GTG	CTT	GAC	CAG	TGG	AAC	CTG	ATG	AGA	CAG	CCC	AGA	CCA	GAC	AGC	1653
Leu	Val	Leu	Asp	Gln	Trp	Asn	Leu	Met	Arg	Gln	Pro	Arg	Pro	Asp	Ser	
	500					505					510					
GAG	GAG	TTC	AAA	TCA	ATT	GAG	GAC	AAG	CTA	GGT	ATC	AAC	TTT	AAG	ATT	1701
Glu	Glu	Phe	Lys	Ser	Ile	Glu	Asp	Lys	Leu	Gly	Ile	Asn	Phe	Lys	Ile	
515					520					525					530	
GAG	AGG	TCC	ATT	GAT	GAT	ATC	AGG	GGC	AAG	CTG	AGA	CAG	CTT	GTC	CTC	1749
Glu	Arg	Ser	Ile	Asp	Asp	Ile	Arg	Gly	Lys	Leu	Arg	Gln	Leu	Val	Leu	
				535					540					545		

CTT	GCA	CAA	CCA	GGG	TAC	CTG	AGT	GGG	GGG	GTT	GAA	CCA	GAA	CAA	TCC	1797
Leu	Ala	Gln	Pro	Gly	Tyr	Leu	Ser	Gly	Gly	Val	Glu	Pro	Glu	Gln	Ser	
			550					555					560			
AGC	CCA	ACT	GTT	GAG	CTT	GAC	CTA	CTA	GGG	TGG	TCA	GCT	ACA	TAC	AGC	1845
Ser	Pro	Thr	Val	Glu	Leu	Asp	Leu	Leu	Gly	Trp	Ser	Ala	Thr	Tyr	Ser	
			565				570					575				
AAA	GAT	CTC	GGG	ATC	TAT	GTG	CCG	GTG	CTT	GAC	AAG	GAA	CGC	CTA	TTT	1893
Lys	Asp	Leu	Gly	Ile	Tyr	Val	Pro	Val	Leu	Asp	Lys	Glu	Arg	Leu	Phe	
	580					585					590					
TGT	TCT	GCT	GCG	TAT	CCC	AAG	GGA	GTA	GAG	AAC	AAG	AGT	CTC	AAG	TCC	1941
Cys	Ser	Ala	Ala	Tyr	Pro	Lys	Gly	Val	Glu	Asn	Lys	Ser	Leu	Lys	Ser	
595					600					605					610	
AAA	GTC	GGG	ATC	GAG	CAG	GCA	TAC	AAG	GTA	GTC	AGG	TAT	GAG	GCG	TTG	1989
Lys	Val	Gly	Ile	Glu	Gln	Ala	Tyr	Lys	Val	Val	Arg	Tyr	Glu	Ala	Leu	
			615						620				625			
AGG	TTG	GTA	GGT	GGT	TGG	AAC	TAC	CCA	CTC	CTG	AAC	AAA	GCC	TGC	AAG	2037
Arg	Leu	Val	Gly	Gly	Trp	Asn	Tyr	Pro	Leu	Leu	Asn	Lys	Ala	Cys	Lys	
			630					635					640			
AAT	AAC	GCA	GGC	GCC	GCT	CGG	CGG	CAT	CTG	GAG	GCC	AAG	GGG	TTC	CCA	2085
Asn	Asn	Ala	Gly	Ala	Ala	Arg	Arg	His	Leu	Glu	Ala	Lys	Gly	Phe	Pro	
		645					650					655				
CTC	GAC	GAG	TTC	CTA	GCC	GAG	TGG	TCT	GAG	CTG	TCA	GAG	TTC	GGT	GAG	2133
Leu	Asp	Glu	Phe	Leu	Ala	Glu	Trp	Ser	Glu	Leu	Ser	Glu	Phe	Gly	Glu	
	660					665					670					
GCC	TTC	GAA	GGC	TTC	AAT	ATC	AAG	CTG	ACC	GTA	ACA	TCT	GAG	AGC	CTA	2181
Ala	Phe	Glu	Gly	Phe	Asn	Ile	Lys	Leu	Thr	Val	Thr	Ser	Glu	Ser	Leu	
675					680					685					690	
GCC	GAA	CTG	AAC	AAG	CCA	GTA	CCC	CCC	AAG	CCC	CCA	AAT	GTC	AAC	AGA	2229
Ala	Glu	Leu	Asn	Lys	Pro	Val	Pro	Pro	Lys	Pro	Pro	Asn	Val	Asn	Arg	
				695					700					705		
CCA	GTC	AAC	ACT	GGG	GGA	CTC	AAG	GCA	GTC	AGC	AAC	GCC	CTC	AAG	ACC	2277
Pro	Val	Asn	Thr	Gly	Gly	Leu	Lys	Ala	Val	Ser	Asn	Ala	Leu	Lys	Thr	
			710					715					720			
GGT	CGG	TAC	AGG	AAC	GAA	GCC	GGA	CTG	AGT	GGT	CTC	GTC	CTT	CTA	GCC	2325
Gly	Arg	Tyr	Arg	Asn	Glu	Ala	Gly	Leu	Ser	Gly	Leu	Val	Leu	Leu	Ala	
		725					730					735				
ACA	GCA	AGA	AGC	CGT	CTG	CAA	GAT	GCA	GTT	AAG	GCC	AAG	GCA	GAA	GCC	2373
Thr	Ala	Arg	Ser	Arg	Leu	Gln	Asp	Ala	Val	Lys	Ala	Lys	Ala	Glu	Ala	
	740					745					750					

GAG AAA CTC CAC AAG TCC AAG CCA GAC GAC CCC GAT GCA GAC TGG TTC	2421
Glu Lys Leu His Lys Ser Lys Pro Asp Asp Pro Asp Ala Asp Trp Phe	
755 760 765 770	
GAA AGA TCA GAA ACT CTG TCA GAC CTT CTG GAG AAA GCC GAC ATC GCC	2469
Glu Arg Ser Glu Thr Leu Ser Asp Leu Leu Glu Lys Ala Asp Ile Ala	
775 780 785	
AGC AAG GTC GCC CAC TCA GCA CTC GTG GAA ACA AGC GAC GCC CTT GAA	2517
Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala Leu Glu	
790 795 800	
GCA GTT CAG TCG ACT TCC GTG TAC ACC CCC AAG TAC CCA GAA GTC AAG	2565
Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu Val Lys	
805 810 815	
AAC CCA CAG ACC GCC TCC AAC CCC GTT GTT GGG CTC CAC CTG CCC GCC	2613
Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu Pro Ala	
820 825 830	
AAG AGA GCC ACC GGT GTC CAG GCC GCT CTT CTC GGA GCA GGA ACG AGC	2661
Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly Thr Ser	
835 840 845 850	
AGA CCA ATG GGG ATG GAG GCC CCA ACA CGG TCC AAG AAC GCC GTG AAA	2709
Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala Val Lys	
855 860 865	
ATG GCC AAA CGG CGG CAA CGC CAA AAG GAG AGC CGC TAACAGCCAT	2755
Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg	
870 875	
GATGGGAACC ACTCAAGAAG AGGACACTAA TCCCAGACCC CGTATCCCCG GCCTTCGCCT	2815
GCGGGGGCCCC CC	2827

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 878 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Ser Asp Ile Phe Asn Ser Pro Gln Ala Arg Ser Thr Ile Ser Ala  
1 5 10 15  
Ala Phe Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu

34

20	25	30
Ile Pro Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser 35 40 45		
Arg Leu Ala Lys Phe Leu Arg Glu Asn Gly Tyr Lys Val Leu Gln Pro 50 55 60		
Arg Ser Leu Pro Glu Asn Glu Glu Tyr Glu Thr Asp Gln Ile Leu Pro 65 70 75 80		
Asp Leu Ala Trp Met Arg Gln Ile Glu Gly Ala Val Leu Lys Pro Thr 85 90 95		
Leu Ser Leu Pro Ile Gly Asp Gln Glu Tyr Phe Pro Lys Tyr Tyr Pro 100 105 110		
Thr His Arg Pro Ser Lys Glu Lys Pro Asn Ala Tyr Pro Pro Asp Ile 115 120 125		
Ala Leu Leu Lys Gln Met Ile Tyr Leu Phe Leu Gln Val Pro Glu Ala 130 135 140		
Asn Glu Gly Leu Lys Asp Glu Val Thr Leu Leu Thr Gln Asn Ile Arg 145 150 155 160		
Asp Lys Ala Tyr Gly Ser Gly Thr Tyr Met Gly Gln Ala Asn Arg Leu 165 170 175		
Val Ala Met Lys Glu Val Ala Thr Gly Arg Asn Pro Asn Lys Asp Pro 180 185 190		
Leu Lys Leu Gly Tyr Thr Phe Glu Ser Ile Ala Gln Leu Leu Asp Ile 195 200 205		
Thr Leu Pro Val Gly Pro Pro Gly Glu Asp Asp Lys Pro Trp Val Pro 210 215 220		
Leu Thr Arg Val Pro Ser Arg Met Leu Val Leu Thr Gly Asp Val Asp 225 230 235 240		
Gly Asp Phe Glu Val Glu Asp Tyr Leu Pro Lys Ile Asn Leu Lys Ser 245 250 255		
Ser Ser Gly Leu Pro Tyr Val Gly Arg Thr Lys Gly Glu Thr Ile Gly 260 265 270		
Glu Met Ile Ala Ile Ser Asn Gln Phe Leu Arg Glu Leu Ser Thr Leu 275 280 285		
Leu Lys Gln Gly Ala Gly Thr Lys Gly Ser Asn Lys Lys Lys Leu Leu		

290		295		300
Ser Met Leu Ser Asp Tyr Trp Tyr Leu Ser Cys Gly Leu Leu Phe Pro				
305		310		315 320
Lys Ala Glu Arg Tyr Asp Lys Ser Thr Trp Leu Thr Lys Thr Arg Asn				
	325		330	335
Ile Trp Ser Ala Pro Ser Pro Thr His Leu Met Ile Ser Met Ile Thr				
	340		345	350
Trp Pro Val Met Ser Asn Ser Pro Asn Asn Val Leu Asn Ile Glu Gly				
	355		360	365
Cys Pro Ser Leu Tyr Lys Phe Asn Pro Phe Arg Gly Gly Leu Asn Arg				
	370		375	380
Ile Val Glu Trp Ile Leu Ala Pro Glu Glu Pro Lys Ala Leu Val Tyr				
385		390		395 400
Ala Asp Asn Ile Tyr Ile Val His Ser Asn Thr Trp Tyr Ser Ile Asp				
	405		410	415
Leu Glu Lys Gly Glu Ala Asn Cys Thr Arg Gln His Met Gln Ala Ala				
	420		425	430
Met Tyr Tyr Ile Leu Thr Arg Gly Trp Ser Asp Asn Gly Asp Pro Met				
	435		440	445
Phe Asn Gln Thr Trp Ala Thr Phe Ala Met Asn Ile Ala Pro Ala Leu				
	450		455	460
Val Val Asp Ser Ser Cys Leu Ile Met Asn Leu Gln Ile Lys Thr Tyr				
465		470		475 480
Gly Gln Gly Ser Gly Asn Ala Ala Thr Phe Ile Asn Asn His Leu Leu				
	485		490	495
Ser Thr Leu Val Leu Asp Gln Trp Asn Leu Met Arg Gln Pro Arg Pro				
	500		505	510
Asp Ser Glu Glu Phe Lys Ser Ile Glu Asp Lys Leu Gly Ile Asn Phe				
	515		520	525
Lys Ile Glu Arg Ser Ile Asp Asp Ile Arg Gly Lys Leu Arg Gln Leu				
	530		535	540
Val Leu Leu Ala Gln Pro Gly Tyr Leu Ser Gly Gly Val Glu Pro Glu				
545		550		555 560
Gln Ser Ser Pro Thr Val Glu Leu Asp Leu Leu Gly Trp Ser Ala Thr				

				565						570					575	
Tyr	Ser	Lys	Asp	Leu	Gly	Ile	Tyr	Val	Pro	Val	Leu	Asp	Lys	Glu	Arg	
			580					585					590			
Leu	Phe	Cys	Ser	Ala	Ala	Tyr	Pro	Lys	Gly	Val	Glu	Asn	Lys	Ser	Leu	
		595					600					605				
Lys	Ser	Lys	Val	Gly	Ile	Glu	Gln	Ala	Tyr	Lys	Val	Val	Arg	Tyr	Glu	
	610					615					620					
Ala	Leu	Arg	Leu	Val	Gly	Gly	Trp	Asn	Tyr	Pro	Leu	Leu	Asn	Lys	Ala	
625					630					635					640	
Cys	Lys	Asn	Asn	Ala	Gly	Ala	Ala	Arg	Arg	His	Leu	Glu	Ala	Lys	Gly	
				645				650						655		
Phe	Pro	Leu	Asp	Glu	Phe	Leu	Ala	Glu	Trp	Ser	Glu	Leu	Ser	Glu	Phe	
			660					665						670		
Gly	Glu	Ala	Phe	Glu	Gly	Phe	Asn	Ile	Lys	Leu	Thr	Val	Thr	Ser	Glu	
		675					680					685				
Ser	Leu	Ala	Glu	Leu	Asn	Lys	Pro	Val	Pro	Pro	Lys	Pro	Pro	Asn	Val	
	690					695					700					
Asn	Arg	Pro	Val	Asn	Thr	Gly	Gly	Leu	Lys	Ala	Val	Ser	Asn	Ala	Leu	
705					710					715					720	
Lys	Thr	Gly	Arg	Tyr	Arg	Asn	Glu	Ala	Gly	Leu	Ser	Gly	Leu	Val	Leu	
				725					730					735		
Leu	Ala	Thr	Ala	Arg	Ser	Arg	Leu	Gln	Asp	Ala	Val	Lys	Ala	Lys	Ala	
			740					745					750			
Glu	Ala	Glu	Lys	Leu	His	Lys	Ser	Lys	Pro	Asp	Asp	Pro	Asp	Ala	Asp	
		755					760					765				
Trp	Phe	Glu	Arg	Ser	Glu	Thr	Leu	Ser	Asp	Leu	Leu	Glu	Lys	Ala	Asp	
	770					775					780					
Ile	Ala	Ser	Lys	Val	Ala	His	Ser	Ala	Leu	Val	Glu	Thr	Ser	Asp	Ala	
785					790					795					800	
Leu	Glu	Ala	Val	Gln	Ser	Thr	Ser	Val	Tyr	Thr	Pro	Lys	Tyr	Pro	Glu	
				805					810					815		
Val	Lys	Asn	Pro	Gln	Thr	Ala	Ser	Asn	Pro	Val	Val	Gly	Leu	His	Leu	
			820					825					830			
Pro	Ala	Lys	Arg	Ala	Thr	Gly	Val	Gln	Ala	Ala	Leu	Leu	Gly	Ala	Gly	

835	840	845
Thr Ser Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala		
850	855	860
Val Lys Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg		
865	870	875

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 97..531

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GGATACGATC GGTCTGACCC CGGGGGAGTC ACCCGGGGAC AGGCCGTCAA GGCCTTGTTTC	60
CAGGATGGGA CTCCTCCTTC TACAACGCTA TCATTG ATG GTT AGT AGA GAT CAG	114
Met Val Ser Arg Asp Gln	880
ACA AAC GAT CGC AGC GAT GAC AAA CCT GCA AGA TCA AAC CCA ACA GAT	162
Thr Asn Asp Arg Ser Asp Asp Lys Pro Ala Arg Ser Asn Pro Thr Asp	885 890 895 900
TGT TCC GTT CAT ACG GAG CCT TCT GAT GCC AAC AAC CGG ACC GGC GTC	210
Cys Ser Val His Thr Glu Pro Ser Asp Ala Asn Asn Arg Thr Gly Val	905 910 915
CAT TCC GGA CGA CAC CCT GGA GAA GCA CAC TCT CAG GTC AGA GAC CTC	258
His Ser Gly Arg His Pro Gly Glu Ala His Ser Gln Val Arg Asp Leu	920 925 930
GAC CTA CAA TTT GAC TGT GGG GGA CAC AGG GTC AGG GCT AAT TGT CTT	306
Asp Leu Gln Phe Asp Cys Gly Gly His Arg Val Arg Ala Asn Cys Leu	935 940 945
TTT CCC TGG ATT CCC TGG CTC AAT TGT GGG TGC TCA CTA CAC ACT GCA	354
Phe Pro Trp Ile Pro Trp Leu Asn Cys Gly Cys Ser Leu His Thr Ala	950 955 960

GGG CAA TGG GAA CTA CAA GTT CGA TCA GAT GCT CCT GAC TGC CCA GAA Gly Gln Trp Glu Leu Gln Val Arg Ser Asp Ala Pro Asp Cys Pro Glu 965 970 975 980	402
CCT ACC GGC CAG TTA CAA CTA CTG CAG GCT AGT GAG TCG GAG TCT CAC Pro Thr Gly Gln Leu Gln Leu Leu Gln Ala Ser Glu Ser Glu Ser His 985 990 995	450
AGT GAG GTC AAG CAC ACT TCC TGG TGG CGT TTA TGC ACT AAA CGG CAC Ser Glu Val Lys His Thr Ser Trp Trp Arg Leu Cys Thr Lys Arg His 1000 1005 1010	498
CAT AAA CGC CGT GAC CTT CCA AGG AAG CCT GAG TGAAGTACATA GATGTTAGCT His Lys Arg Arg Asp Leu Pro Arg Lys Pro Glu 1015 1020	551
ACAATGGGTT GATGTCTGCA ACAGCCAACA TCAACGACAA AATTGGGAAC GTCCTAGTAG	611
GGGAAGGGGT CACCGTCCTC AGCTTACCCA CATCATATGA TCTTGGGTAT GTGAGGCTTG	671
GTGACCCCAT TCCCGCAATA GGGCTTGACC CAAAAATGGT AGCCACATGT GACAGCAGTG	731
ACAGGCCAG AGTCTACACC ATAAGTGCAG CCGATGATTA CCAATTCTCA TCACAGTACC	791
AACCAGGTGG GGTAACAATC AACTGTCTCT CAGCCAACAT TGATGCCATC ACAAGCCTCA	851
GCGTTGGGGG AGAGCTCGTG TTTCAAACAA GCGTCCACGG CTTGTACTG GGCGCCACCA	911
TCTACCTCAT AGGCTTTGAT GGGACAACGG TAATCACCAG GGCTGTGGCC GCAAACAATG	971
GGCTGACGAC CGGCACCGAC AACCTTATGC CATTCAATCT TGTGATTCCA ACAAACGAGA	1031
TAACCCAGCC AATCACATCC ATCAAAGTGG AGATAGTGAC CTCCAAAAGT GGTGGTCAGG	1091
CAGGGGATCA GATGTCATGG TCGGCAAGAG GGAGCCTAGC AGTGACGATC CATGGTGGCA	1151
ACTATCCAGG GGCCCTCCGT CCCGTCACGC TAGTGGCCTA CGAAAGAGTG GCAACAGGAT	1211
CCGTCGTTAC GGTGCTGGG GTGAGCAACT TCGAGCTGAT CCCAAATCCT GAACTAGCAA	1271
AGAACCTGGT TACAGAATAC GGCCGATTTG ACCCAGGAGC CATGAACTAC ACAAATTGA	1331
TACTGAGTGA GAGGGACCGT CTTGGCATCA AGACCGTCTG GCCAACAAGG GAGTACACTG	1391
ACTTTCGTGA ATACTTCATG GAGGTGGCCG ACCTCAACTC TCCCCTGAAG ATTGCAGGAG	1451
CATTCGGCTT CAAAGACATA ATCCGGGCCA TAAGGAGGAT AGCTGTGCCG GTGGTCTCCA	1511
CATTGTTCCC ACCTGCCGCT CCCCTAGCCC ATGCAATTGG GGAAGGTGTA GACTACCTGC	1571
TGGGCGATGA GGCACAGGCT GCTTCAGGAA CTGCTCGAGC CGCGTCAGGA AAAGCAAGAG	1631



CTGCCTCAGG CCGCATAAGG CAGCTGACTC TCGCCGCCGA CAAGGGGTAC GAGGTAGTCG 1691  
CGAATCTATT CCAGGTGCCC CAGAATCCCG TAGTCGACGG GATTCTTGCT TCACCTGGGG 1751  
TACTCCGCGG TGCACACAAC CTCGACTGCG TGTTAAGAGA GGGTGCCACG CTATTCCCTG 1811  
TGGTTATTAC GACAGTGGAA GACGCCATGA CACCCAAAGC ATTGAACAGC AAAATGTTTG 1871  
CTGTCATTGA AGGCGTGCGA GAAGACCTCC AACCTCCATC TCAAAGAGGA TCCTTCATAC 1931  
GAACTCTCTC TGGACACAGA GTCTATGGAT ATGCTCCAGA TGGGGTACTT CCACTGGAGA 1991  
CTGGGAGAGA CTACACCGTT GTCCCAATAG ATGATGTCTG GGACGACAGC ATTATGCTGT 2051  
CCAAAGATCC CATACTCCT ATTGTGGGAA ACAGTGGAAA TCTAGCCATA GCTTACATGG 2111  
ATGTGTTTTG ACCCAAAGTC CCAATCCATG TGGCTATGAC GGGAGCCCTC AATGCTTG TG 2171  
GCGAGATTGA GAAAGTAAGC TTTAGAAGCA CCAAGCTCGC CACTGCACAC CGACTTGGCC 2231  
TTAGGTTGGC TGGTCCCGGA GCATTGATG TAAACACCGG GCCCAACTGG GCAACGTTCA 2291  
TCAAACGTTT CCCTCACAAT CCACGCGACT GGGACAGGCT CCCCTACCTC AACCTACCAT 2351  
ACCTTCCACC CAATGCAGGA CGCCAGTACC ACCTTGCCAT GGCTGCATCA GAGTTCAAAG 2411  
AGACCCCCGA ACTCGAGAGT GCCGTCAGAG CAATGGAAGC AGCAGCCAAC GTGGACCCAC 2471  
TATTCCAATC TGCACTCAGT GTGTTTCATGT GGCTGGAAGA GAATGGGATT GTGACTGACA 2531  
TGGCCAACTT CGCACTCAGC GACCCGAACG CCCATCGGAT GCGAAATTTT CTTGCAAACG 2591  
CACCACAAGC AGGCAGCAAG TCGCAAAGGG CCAAGTACGG GACAGCAGGC TACGGAGTGG 2651  
AGGCTCGGGG CCCCACACCA GAGGAAGCAC AGAGGGAAAA AGACACACGG ATCTCAAAGA 2711  
AGATGGAGAC CATGGGCATC TACTTTGCAA CACCAGAATG GGTAGCACTC AATGGGCACC 2771  
GAGGGCCAAG CCCC GGCCAG CTAAAGTACT GGCAGAACAC ACGAGAAATA CCGGACCCAA 2831  
ACGAGGACTA TCTAGACTAC GTGCATGCAG AGAAGAGCCG GTTGGCATCA GAAGAACAAA 2891  
TCCTAAGGGC AGCTACGTCG ATCTACGGGG CTCCAGGACA GGCAGAGCCA CCCAAGCTT 2951  
TCATAGACGA AGTTGCCAAA GTCTATGAAA TCAACCATGG ACGTGGCCCA AACCAAGAAC 3011  
AGATGAAAGA TCTGCTCTTG ACTGCGATGG AGATGAAGCA TCGCAATCCC AGGCGGGCTC 3071  
TACCAAAGCC CAAGCCAAAA CCCAATGCTC CAACACAGAG ACCCCCTGGT CGGCTGGGCC 3131  
GCTGGATCAG GACCGTCTCT GATGAGGACC TTGAGTGAGG CTCCTGGGAG TCTCCCGACA 3191

40

CCACCCGCGC AGGTGTGGAC ACCAATTCGG CCTTACAACA TCCCAAATTG GATCCGTTCC 3251  
 CGGGTCCCCT 3261

## (2) INFORMATION FOR SEQ ID NO:28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp Asp Lys Pro Ala  
 1 5 10 15  
 Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu Pro Ser Asp Ala  
 20 25 30  
 Asn Asn Arg Thr Gly Val His Ser Gly Arg His Pro Gly Glu Ala His  
 35 40 45  
 Ser Gln Val Arg Asp Leu Asp Leu Gln Phe Asp Cys Gly Gly His Arg  
 50 55 60  
 Val Arg Ala Asn Cys Leu Phe Pro Trp Ile Pro Trp Leu Asn Cys Gly  
 65 70 75 80  
 Cys Ser Leu His Thr Ala Gly Gln Trp Glu Leu Gln Val Arg Ser Asp  
 85 90 95  
 Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln Leu Leu Gln Ala  
 100 105 110  
 Ser Glu Ser Glu Ser His Ser Glu Val Lys His Thr Ser Trp Trp Arg  
 115 120 125  
 Leu Cys Thr Lys Arg His His Lys Arg Arg Asp Leu Pro Arg Lys Pro  
 130 135 140  
 Glu  
 145

## (2) INFORMATION FOR SEQ ID NO:29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 131..3166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

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GGATACGATC GGTCTGACCC CGGGGGAGTC ACCCGGGGAC AGGCCGTCAA GGCCTTGTTT      60
CAGGATGGGA CTCCTCCTTC TACAACGCTA TCATTGATGG TTAGTAGAGA TCAGACAAAC      120
GATCGCAGCG ATG ACA AAC CTG CAA GAT CAA ACC CAA CAG ATT GTT CCG      169
      Met Thr Asn Leu Gln Asp Gln Thr Gln Gln Ile Val Pro
                        150                        155

TTC ATA CGG AGC CTT CTG ATG CCA ACA ACC GGA CCG GCG TCC ATT CCG      217
Phe Ile Arg Ser Leu Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro
      160                        165                        170

GAC GAC ACC CTG GAG AAG CAC ACT CTC AGG TCA GAG ACC TCG ACC TAC      265
Asp Asp Thr Leu Glu Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr
      175                        180                        185                        190

AAT TTG ACT GTG GGG GAC ACA GGG TCA GGG CTA ATT GTC TTT TTC CCT      313
Asn Leu Thr Val Gly Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro
                        195                        200                        205

GGA TTC CCT GGC TCA ATT GTG GGT GCT CAC TAC ACA CTG CAG GGC AAT      361
Gly Phe Pro Gly Ser Ile Val Gly Ala His Tyr Thr Leu Gln Gly Asn
                        210                        215                        220

GGG AAC TAC AAG TTC GAT CAG ATG CTC CTG ACT GCC CAG AAC CTA CCG      409
Gly Asn Tyr Lys Phe Asp Gln Met Leu Leu Thr Ala Gln Asn Leu Pro
                        225                        230                        235

GCC AGT TAC AAC TAC TGC AGG CTA GTG AGT CGG AGT CTC ACA GTG AGG      457
Ala Ser Tyr Asn Tyr Cys Arg Leu Val Ser Arg Ser Leu Thr Val Arg
      240                        245                        250

TCA AGC ACA CTT CCT GGT GGC GTT TAT GCA CTA AAC GGC ACC ATA AAC      505
Ser Ser Thr Leu Pro Gly Gly Val Tyr Ala Leu Asn Gly Thr Ile Asn
      255                        260                        265                        270

GCC GTG ACC TTC CAA GGA AGC CTG AGT GAA CTG ACA GAT GTT AGC TAC      553

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Ala	Val	Thr	Phe	Gln	Gly	Ser	Leu	Ser	Glu	Leu	Thr	Asp	Val	Ser	Tyr	
				275					280					285		
AAT	GGG	TTG	ATG	TCT	GCA	ACA	GCC	AAC	ATC	AAC	GAC	AAA	ATT	GGG	AAC	601
Asn	Gly	Leu	Met	Ser	Ala	Thr	Ala	Asn	Ile	Asn	Asp	Lys	Ile	Gly	Asn	
			290					295					300			
GTC	CTA	GTA	GGG	GAA	GGG	GTC	ACC	GTC	CTC	AGC	TTA	CCC	ACA	TCA	TAT	649
Val	Leu	Val	Gly	Glu	Gly	Val	Thr	Val	Leu	Ser	Leu	Pro	Thr	Ser	Tyr	
		305					310					315				
GAT	CTT	GGG	TAT	GTG	AGG	CTT	GGT	GAC	CCC	ATT	CCC	GCA	ATA	GGG	CTT	697
Asp	Leu	Gly	Tyr	Val	Arg	Leu	Gly	Asp	Pro	Ile	Pro	Ala	Ile	Gly	Leu	
	320					325					330					
GAC	CCA	AAA	ATG	GTA	GCC	ACA	TGT	GAC	AGC	AGT	GAC	AGG	CCC	AGA	GTC	745
Asp	Pro	Lys	Met	Val	Ala	Thr	Cys	Asp	Ser	Ser	Asp	Arg	Pro	Arg	Val	
335					340					345					350	
TAC	ACC	ATA	ACT	GCA	GCC	GAT	GAT	TAC	CAA	TTC	TCA	TCA	CAG	TAC	CAA	793
Tyr	Thr	Ile	Thr	Ala	Ala	Asp	Asp	Tyr	Gln	Phe	Ser	Ser	Gln	Tyr	Gln	
				355					360					365		
CCA	GGT	GGG	GTA	ACA	ATC	ACA	CTG	TTC	TCA	GCC	AAC	ATT	GAT	GCC	ATC	841
Pro	Gly	Gly	Val	Thr	Ile	Thr	Leu	Phe	Ser	Ala	Asn	Ile	Asp	Ala	Ile	
			370					375					380			
ACA	AGC	CTC	AGC	GTT	GGG	GGA	GAG	CTC	GTG	TTT	CAA	ACA	AGC	GTC	CAC	889
Thr	Ser	Leu	Ser	Val	Gly	Gly	Glu	Leu	Val	Phe	Gln	Thr	Ser	Val	His	
		385					390					395				
GGC	CTT	GTA	CTG	GGC	GCC	ACC	ATC	TAC	CTC	ATA	GGC	TTT	GAT	GGG	ACA	937
Gly	Leu	Val	Leu	Gly	Ala	Thr	Ile	Tyr	Leu	Ile	Gly	Phe	Asp	Gly	Thr	
	400					405					410					
ACG	GTA	ATC	ACC	AGG	GCT	GTG	GCC	GCA	AAC	AAT	GGG	CTG	ACG	ACC	GGC	985
Thr	Val	Ile	Thr	Arg	Ala	Val	Ala	Ala	Asn	Asn	Gly	Leu	Thr	Thr	Gly	
415					420				425						430	
ACC	GAC	AAC	CTT	ATG	CCA	TTC	AAT	CTT	GTG	ATT	CCA	ACA	AAC	GAG	ATA	1033
Thr	Asp	Asn	Leu	Met	Pro	Phe	Asn	Leu	Val	Ile	Pro	Thr	Asn	Glu	Ile	
				435					440					445		
ACC	CAG	CCA	ATC	ACA	TCC	ATC	AAA	CTG	GAG	ATA	GTG	ACC	TCC	AAA	AGT	1081
Thr	Gln	Pro	Ile	Thr	Ser	Ile	Lys	Leu	Glu	Ile	Val	Thr	Ser	Lys	Ser	
			450					455					460			
GGT	GGT	CAG	GCA	GGG	GAT	CAG	ATG	TCA	TGG	TCG	GCA	AGA	GGG	AGC	CTA	1129
Gly	Gly	Gln	Ala	Gly	Asp	Gln	Met	Ser	Trp	Ser	Ala	Arg	Gly	Ser	Leu	
		465					470					475				

GCA	GTG	ACG	ATC	CAT	GGT	GGC	AAC	TAT	CCA	GGG	GCC	CTC	CGT	CCC	GTC	1177
Ala	Val	Thr	Ile	His	Gly	Gly	Asn	Tyr	Pro	Gly	Ala	Leu	Arg	Pro	Val	
480						485					490					
ACG	CTA	GTG	GCC	TAC	GAA	AGA	GTG	GCA	ACA	GGA	TCC	GTC	GTT	ACG	GTC	1225
Thr	Leu	Val	Ala	Tyr	Glu	Arg	Val	Ala	Thr	Gly	Ser	Val	Val	Thr	Val	
495					500					505					510	
GCT	GGG	GTG	AGC	AAC	TTC	GAG	CTG	ATC	CCA	AAT	CCT	GAA	CTA	GCA	AAG	1273
Ala	Gly	Val	Ser	Asn	Phe	Glu	Leu	Ile	Pro	Asn	Pro	Glu	Leu	Ala	Lys	
				515					520					525		
AAC	CTG	GTT	ACA	GAA	TAC	GGC	CGA	TTT	GAC	CCA	GGA	GCC	ATG	AAC	TAC	1321
Asn	Leu	Val	Thr	Glu	Tyr	Gly	Arg	Phe	Asp	Pro	Gly	Ala	Met	Asn	Tyr	
			530					535					540			
ACA	AAA	TTG	ATA	CTG	AGT	GAG	AGG	GAC	CGT	CTT	GGC	ATC	AAG	ACC	GTC	1369
Thr	Lys	Leu	Ile	Leu	Ser	Glu	Arg	Asp	Arg	Leu	Gly	Ile	Lys	Thr	Val	
	545						550					555				
TGG	CCA	ACA	AGG	GAG	TAC	ACT	GAC	TTT	CGT	GAA	TAC	TTC	ATG	GAG	GTG	1417
Trp	Pro	Thr	Arg	Glu	Tyr	Thr	Asp	Phe	Arg	Glu	Tyr	Phe	Met	Glu	Val	
	560					565					570					
GCC	GAC	CTC	AAC	TCT	CCC	CTG	AAG	ATT	GCA	GGA	GCA	TTC	GGC	TTC	AAA	1465
Ala	Asp	Leu	Asn	Ser	Pro	Leu	Lys	Ile	Ala	Gly	Ala	Phe	Gly	Phe	Lys	
575					580					585					590	
GAC	ATA	ATC	CGG	GCC	ATA	AGG	AGG	ATA	GCT	GTG	CCG	GTG	GTC	TCC	ACA	1513
Asp	Ile	Ile	Arg	Ala	Ile	Arg	Arg	Ile	Ala	Val	Pro	Val	Val	Ser	Thr	
				595					600					605		
TTG	TTC	CCA	CCT	GCC	GCT	CCC	CTA	GCC	CAT	GCA	ATT	GGG	GAA	GGT	GTA	1561
Leu	Phe	Pro	Pro	Ala	Ala	Pro	Leu	Ala	His	Ala	Ile	Gly	Glu	Gly	Val	
			610					615					620			
GAC	TAC	CTG	CTG	GGC	GAT	GAG	GCA	CAG	GCT	GCT	TCA	GGA	ACT	GCT	CGA	1609
Asp	Tyr	Leu	Leu	Gly	Asp	Glu	Ala	Gln	Ala	Ala	Ser	Gly	Thr	Ala	Arg	
		625					630					635				
GCC	GCG	TCA	GGA	AAA	GCA	AGA	GCT	GCC	TCA	GGC	CGC	ATA	AGG	CAG	CTG	1657
Ala	Ala	Ser	Gly	Lys	Ala	Arg	Ala	Ala	Ser	Gly	Arg	Ile	Arg	Gln	Leu	
	640					645					650					
ACT	CTC	GCC	GCC	GAC	AAG	GGG	TAC	GAG	GTA	GTC	GCG	AAT	CTA	TTC	CAG	1705
Thr	Leu	Ala	Ala	Asp	Lys	Gly	Tyr	Glu	Val	Val	Ala	Asn	Leu	Phe	Gln	
655					660					665					670	
GTG	CCC	CAG	AAT	CCC	GTA	GTC	GAC	GGG	ATT	CTT	GCT	TCA	CCT	GGG	GTA	1753
Val	Pro	Gln	Asn	Pro	Val	Val	Asp	Gly	Ile	Leu	Ala	Ser	Pro	Gly	Val	
				675					680					685		

CTC	CGC	GGT	GCA	CAC	AAC	CTC	GAC	TGC	GTG	TTA	AGA	GAG	GGT	GCC	ACG	1801
Leu	Arg	Gly	Ala	His	Asn	Leu	Asp	Cys	Val	Leu	Arg	Glu	Gly	Ala	Thr	
			690					695					700			
CTA	TTC	CCT	GTG	GTT	ATT	ACG	ACA	GTG	GAA	GAC	GCC	ATG	ACA	CCC	AAA	1849
Leu	Phe	Pro	Val	Val	Ile	Thr	Thr	Val	Glu	Asp	Ala	Met	Thr	Pro	Lys	
		705					710					715				
GCA	TTG	AAC	AGC	AAA	ATG	TTT	GCT	GTC	ATT	GAA	GGC	GTG	CGA	GAA	GAC	1897
Ala	Leu	Asn	Ser	Lys	Met	Phe	Ala	Val	Ile	Glu	Gly	Val	Arg	Glu	Asp	
	720					725					730					
CTC	CAA	CCT	CCA	TCT	CAA	AGA	GGA	TCC	TTC	ATA	CGA	ACT	CTC	TCT	GGA	1945
Leu	Gln	Pro	Pro	Ser	Gln	Arg	Gly	Ser	Phe	Ile	Arg	Thr	Leu	Ser	Gly	
735					740					745					750	
CAC	AGA	GTC	TAT	GGA	TAT	GCT	CCA	GAT	GGG	GTA	CTT	CCA	CTG	GAG	ACT	1993
His	Arg	Val	Tyr	Gly	Tyr	Ala	Pro	Asp	Gly	Val	Leu	Pro	Leu	Glu	Thr	
			755						760					765		
GGG	AGA	GAC	TAC	ACC	GTT	GTC	CCA	ATA	GAT	GAT	GTC	TGG	GAC	GAC	AGC	2041
Gly	Arg	Asp	Tyr	Thr	Val	Val	Pro	Ile	Asp	Asp	Val	Trp	Asp	Asp	Ser	
		770					775						780			
ATT	ATG	CTG	TCC	AAA	GAT	CCC	ATA	CCT	CCT	ATT	GTG	GGA	AAC	AGT	GGA	2089
Ile	Met	Leu	Ser	Lys	Asp	Pro	Ile	Pro	Pro	Ile	Val	Gly	Asn	Ser	Gly	
		785					790					795				
AAT	CTA	GCC	ATA	GCT	TAC	ATG	GAT	GTG	TTT	CGA	CCC	AAA	GTC	CCA	ATC	2137
Asn	Leu	Ala	Ile	Ala	Tyr	Met	Asp	Val	Phe	Arg	Pro	Lys	Val	Pro	Ile	
	800					805					810					
CAT	GTG	GCT	ATG	ACG	GGA	GCC	CTC	AAT	GCT	TGT	GGC	GAG	ATT	GAG	AAA	2185
His	Val	Ala	Met	Thr	Gly	Ala	Leu	Asn	Ala	Cys	Gly	Glu	Ile	Glu	Lys	
815					820					825					830	
GTA	AGC	TTT	AGA	AGC	ACC	AAG	CTC	GCC	ACT	GCA	CAC	CGA	CTT	GGC	CTT	2233
Val	Ser	Phe	Arg	Ser	Thr	Lys	Leu	Ala	Thr	Ala	His	Arg	Leu	Gly	Leu	
				835					840					845		
AGG	TTG	GCT	GGT	CCC	GGA	GCA	TTC	GAT	GTA	AAC	ACC	GGG	CCC	AAC	TGG	2281
Arg	Leu	Ala	Gly	Pro	Gly	Ala	Phe	Asp	Val	Asn	Thr	Gly	Pro	Asn	Trp	
		850						855					860			
GCA	ACG	TTC	ATC	AAA	CGT	TTC	CCT	CAC	AAT	CCA	CGC	GAC	TGG	GAC	AGG	2329
Ala	Thr	Phe	Ile	Lys	Arg	Phe	Pro	His	Asn	Pro	Arg	Asp	Trp	Asp	Arg	
		865					870					875				
CTC	CCC	TAC	CTC	AAC	CTA	CCA	TAC	CTT	CCA	CCC	AAT	GCA	GGA	CGC	CAG	2377
Leu	Pro	Tyr	Leu	Asn	Leu	Pro	Tyr	Leu	Pro	Pro	Asn	Ala	Gly	Arg	Gln	
	880					885					890					

## 45

TAC CAC CTT GCC ATG GCT GCA TCA GAG TTC AAA GAG ACC CCC GAA CTC	2425
Tyr His Leu Ala Met Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu	
895 900 905 910	
GAG AGT GCC GTC AGA GCA ATG GAA GCA GCA GCC AAC GTG GAC CCA CTA	2473
Glu Ser Ala Val Arg Ala Met Glu Ala Ala Ala Asn Val Asp Pro Leu	
915 920 925	
TTC CAA TCT GCA CTC AGT GTG TTC ATG TGG CTG GAA GAG AAT GGG ATT	2521
Phe Gln Ser Ala Leu Ser Val Phe Met Trp Leu Glu Glu Asn Gly Ile	
930 935 940	
GTG ACT GAC ATG GCC AAC TTC GCA CTC AGC GAC CCG AAC GCC CAT CGG	2569
Val Thr Asp Met Ala Asn Phe Ala Leu Ser Asp Pro Asn Ala His Arg	
945 950 955	
ATG CGA AAT TTT CTT GCA AAC GCA CCA CAA GCA GGC AGC AAG TCG CAA	2617
Met Arg Asn Phe Leu Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln	
960 965 970	
AGG GCC AAG TAC GGG ACA GCA GGC TAC GGA GTG GAG GCT CGG GGC CCC	2665
Arg Ala Lys Tyr Gly Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro	
975 980 985 990	
ACA CCA GAG GAA GCA CAG AGG GAA AAA GAC ACA CGG ATC TCA AAG AAG	2713
Thr Pro Glu Glu Ala Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys	
995 1000 1005	
ATG GAG ACC ATG GGC ATC TAC TTT GCA ACA CCA GAA TGG GTA GCA CTC	2761
Met Glu Thr Met Gly Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu	
1010 1015 1020	
AAT GGG CAC CGA GGG CCA AGC CCC GGC CAG CTA AAG TAC TGG CAG AAC	2809
Asn Gly His Arg Gly Pro Ser Pro Gly Gln Leu Lys Tyr Trp Gln Asn	
1025 1030 1035	
ACA CGA GAA ATA CCG GAC CCA AAC GAG GAC TAT CTA GAC TAC GTG CAT	2857
Thr Arg Glu Ile Pro Asp Pro Asn Glu Asp Tyr Leu Asp Tyr Val His	
1040 1045 1050	
GCA GAG AAG AGC CGG TTG GCA TCA GAA GAA CAA ATC CTA AGG GCA GCT	2905
Ala Glu Lys Ser Arg Leu Ala Ser Glu Glu Gln Ile Leu Arg Ala Ala	
1055 1060 1065 1070	
ACG TCG ATC TAC GGG GCT CCA GGA CAG GCA GAG CCA CCC CAA GCT TTC	2953
Thr Ser Ile Tyr Gly Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe	
1075 1080 1085	
ATA GAC GAA GTT GCC AAA GTC TAT GAA ATC AAC CAT GGA CGT GGC CCA	3001
Ile Asp Glu Val Ala Lys Val Tyr Glu Ile Asn His Gly Arg Gly Pro	
1090 1095 1100	

46

AAC CAA GAA CAG ATG AAA GAT CTG CTC TTG ACT GCG ATG GAG ATG AAG 3049  
 Asn Gln Glu Gln Met Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys  
 1105 1110 1115

CAT CGC AAT CCC AGG CGG GCT CTA CCA AAG CCC AAG CCA AAA CCC AAT 3097  
 His Arg Asn Pro Arg Arg Ala Leu Pro Lys Pro Lys Pro Lys Pro Asn  
 1120 1125 1130

GCT CCA ACA CAG AGA CCC CCT GGT CGG CTG GGC CGC TGG ATC AGG ACC 3145  
 Ala Pro Thr Gln Arg Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Thr  
 1135 1140 1145 1150

GTC TCT GAT GAG GAC CTT GAG TGAGGCTCCT GGGAGTCTCC CGACACCACC 3196  
 Val Ser Asp Glu Asp Leu Glu  
 1155

CGCGCAGGTG TGGACACCAA TTCGGCCTTA CAACATCCCA AATTGGATCC GTTCGCGGGT 3256  
 CCCCT 3261

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1012 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Thr Asn Leu Gln Asp Gln Thr Gln Gln Ile Val Pro Phe Ile Arg  
 1 5 10 15

Ser Leu Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro Asp Asp Thr  
 20 25 30

Leu Glu Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr Asn Leu Thr  
 35 40 45

Val Gly Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro Gly Phe Pro  
 50 55 60

Gly Ser Ile Val Gly Ala His Tyr Thr Leu Gln Gly Asn Gly Asn Tyr  
 65 70 75 80

Lys Phe Asp Gln Met Leu Leu Thr Ala Gln Asn Leu Pro Ala Ser Tyr  
 85 90 95

Asn Tyr Cys Arg Leu Val Ser Arg Ser Leu Thr Val Arg Ser Ser Thr  
 100 105 110



Leu Pro Gly Gly Val Tyr Ala Leu Asn Gly Thr Ile Asn Ala Val Thr  
 115 120 125  
 Phe Gln Gly Ser Leu Ser Glu Leu Thr Asp Val Ser Tyr Asn Gly Leu  
 130 135 140  
 Met Ser Ala Thr Ala Asn Ile Asn Asp Lys Ile Gly Asn Val Leu Val  
 145 150 155 160  
 Gly Glu Gly Val Thr Val Leu Ser Leu Pro Thr Ser Tyr Asp Leu Gly  
 165 170 175  
 Tyr Val Arg Leu Gly Asp Pro Ile Pro Ala Ile Gly Leu Asp Pro Lys  
 180 185 190  
 Met Val Ala Thr Cys Asp Ser Ser Asp Arg Pro Arg Val Tyr Thr Ile  
 195 200 205  
 Thr Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Pro Gly Gly  
 210 215 220  
 Val Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu  
 225 230 235 240  
 Ser Val Gly Gly Glu Leu Val Phe Gln Thr Ser Val His Gly Leu Val  
 245 250 255  
 Leu Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Thr Val Ile  
 260 265 270  
 Thr Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn  
 275 280 285  
 Leu Met Pro Phe Asn Leu Val Ile Pro Thr Asn Glu Ile Thr Gln Pro  
 290 295 300  
 Ile Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln  
 305 310 315 320  
 Ala Gly Asp Gln Met Ser Trp Ser Ala Arg Gly Ser Leu Ala Val Thr  
 325 330 335  
 Ile His Gly Gly Asn Tyr Pro Gly Ala Leu Arg Pro Val Thr Leu Val  
 340 345 350  
 Ala Tyr Glu Arg Val Ala Thr Gly Ser Val Val Thr Val Ala Gly Val  
 355 360 365  
 Ser Asn Phe Glu Leu Ile Pro Asn Pro Glu Leu Ala Lys Asn Leu Val  
 370 375 380  
 Thr Glu Tyr Gly Arg Phe Asp Pro Gly Ala Met Asn Tyr Thr Lys Leu

385		390		395		400
Ile Leu Ser Glu Arg Asp Arg Leu Gly Ile Lys Thr Val Trp Pro Thr						
	405		410		415	
Arg Glu Tyr Thr Asp Phe Arg Glu Tyr Phe Met Glu Val Ala Asp Leu						
	420		425		430	
Asn Ser Pro Leu Lys Ile Ala Gly Ala Phe Gly Phe Lys Asp Ile Ile						
	435		440		445	
Arg Ala Ile Arg Arg Ile Ala Val Pro Val Val Ser Thr Leu Phe Pro						
	450		455		460	
Pro Ala Ala Pro Leu Ala His Ala Ile Gly Glu Gly Val Asp Tyr Leu						
	465		470		475	480
Leu Gly Asp Glu Ala Gln Ala Ala Ser Gly Thr Ala Arg Ala Ala Ser						
	485		490		495	
Gly Lys Ala Arg Ala Ala Ser Gly Arg Ile Arg Gln Leu Thr Leu Ala						
	500		505		510	
Ala Asp Lys Gly Tyr Glu Val Val Ala Asn Leu Phe Gln Val Pro Gln						
	515		520		525	
Asn Pro Val Val Asp Gly Ile Leu Ala Ser Pro Gly Val Leu Arg Gly						
	530		535		540	
Ala His Asn Leu Asp Cys Val Leu Arg Glu Gly Ala Thr Leu Phe Pro						
	545		550		555	560
Val Val Ile Thr Thr Val Glu Asp Ala Met Thr Pro Lys Ala Leu Asn						
	565		570		575	
Ser Lys Met Phe Ala Val Ile Glu Gly Val Arg Glu Asp Leu Gln Pro						
	580		585		590	
Pro Ser Gln Arg Gly Ser Phe Ile Arg Thr Leu Ser Gly His Arg Val						
	595		600		605	
Tyr Gly Tyr Ala Pro Asp Gly Val Leu Pro Leu Glu Thr Gly Arg Asp						
	610		615		620	
Tyr Thr Val Val Pro Ile Asp Asp Val Trp Asp Asp Ser Ile Met Leu						
	625		630		635	640
Ser Lys Asp Pro Ile Pro Pro Ile Val Gly Asn Ser Gly Asn Leu Ala						
	645		650		655	
Ile Ala Tyr Met Asp Val Phe Arg Pro Lys Val Pro Ile His Val Ala						
	660		665		670	

Met Thr Gly Ala Leu Asn Ala Cys Gly Glu Ile Glu Lys Val Ser Phe  
 675 680 685

Arg Ser Thr Lys Leu Ala Thr Ala His Arg Leu Gly Leu Arg Leu Ala  
 690 695 700

Gly Pro Gly Ala Phe Asp Val Asn Thr Gly Pro Asn Trp Ala Thr Phe  
 705 710 715 720

Ile Lys Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg Leu Pro Tyr  
 725 730 735

Leu Asn Leu Pro Tyr Leu Pro Pro Asn Ala Gly Arg Gln Tyr His Leu  
 740 745 750

Ala Met Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu Glu Ser Ala  
 755 760 765

Val Arg Ala Met Glu Ala Ala Ala Asn Val Asp Pro Leu Phe Gln Ser  
 770 775 780

Ala Leu Ser Val Phe Met Trp Leu Glu Glu Asn Gly Ile Val Thr Asp  
 785 790 795 800

Met Ala Asn Phe Ala Leu Ser Asp Pro Asn Ala His Arg Met Arg Asn  
 805 810 815

Phe Leu Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys  
 820 825 830

Tyr Gly Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu  
 835 840 845

Glu Ala Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr  
 850 855 860

Met Gly Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His  
 865 870 875 880

Arg Gly Pro Ser Pro Gly Gln Leu Lys Tyr Trp Gln Asn Thr Arg Glu  
 885 890 895

Ile Pro Asp Pro Asn Glu Asp Tyr Leu Asp Tyr Val His Ala Glu Lys  
 900 905 910

Ser Arg Leu Ala Ser Glu Glu Gln Ile Leu Arg Ala Ala Thr Ser Ile  
 915 920 925

Tyr Gly Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu  
 930 935 940

Val Ala Lys Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu

[illegible]

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3264 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA

(ix) **FEATURE:**

- (A) NAME/KEY: CDS  
(B) LOCATION: 97..531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GGATACGATC GGTCTGACCC CGGGGGAGTC ACCCGGGGAC AGGCCATCAC TGCCTTGTTT	60
CTGGTTGGAA CTCCTCTTTC TGCTGTACTA TCGTTG ATG GTG AGT AGA GAT CAG	114
Met Val Ser Arg Asp Gln	
1015	
ACA AAC GAT CGC AGC GAT GAC AAA CCT GAT GGA TCA CAC CCA ACA GAT	162
Thr Asn Asp Arg Ser Asp Asp Lys Pro Asp Gly Ser His Pro Thr Asp	
1020 1025 1030	
TGT TCC GTT CAT ACG GAG CCT TCT GAT GCC AAC GAC CGG ACC GGC GTC	210
Cys Ser Val His Thr Glu Pro Ser Asp Ala Asn Asp Arg Thr Gly Val	
1035 1040 1045 1050	
CAT TCC GGA CGA CAC CCT GGA GAA GCA CAC ACT CAG GTC CGA AAC CTC	258
His Ser Gly Arg His Pro Gly Glu Ala His Thr Gln Val Arg Asn Leu	
1055 1060 1065	
GAC TTA CAA CTT GAC TGT AGG GGA TAC AGG GTC AGG ACT AAT TGT CTT	306

Asp	Leu	Gln	Leu	Asp	Cys	Arg	Gly	Tyr	Arg	Val	Arg	Thr	Asn	Cys	Leu		
1070				1075				1080									
TTT	CCC	TGG	ATT	CCC	TGG	TTC	AGT	TGT	AGG	TGC	TCA	CTA	CAC	ACT	GCA	354	
Phe	Pro	Trp	Ile	Pro	Trp	Phe	Ser	Cys	Arg	Cys	Ser	Leu	His	Thr	Ala		
1085				1090				1095									
GAG	CAG	TGG	GAA	CTA	CCA	ATT	CGA	CCA	GAT	GCT	CCT	GAC	AGC	GCA	GAA	402	
Glu	Gln	Trp	Glu	Leu	Pro	Ile	Arg	Pro	Asp	Ala	Pro	Asp	Ser	Ala	Glu		
1100				1105				1110									
CCT	GCC	TGC	CAG	CTA	CAA	CTA	CTG	CAG	GCT	AGT	GAG	CAG	GAG	TCT	AAC	450	
Pro	Ala	Cys	Gln	Leu	Gln	Leu	Leu	Gln	Ala	Ser	Glu	Gln	Glu	Ser	Asn		
1115				1120				1125								1130	
CGT	ACG	GTC	AAG	CAC	ACT	CCC	TGG	TGG	CGT	TTA	TGC	ACT	AAA	CGG	AAC	498	
Arg	Thr	Val	Lys	His	Thr	Pro	Trp	Trp	Arg	Leu	Cys	Thr	Lys	Arg	Asn		
1135				1140				1145									
CAT	AAA	CGC	AGT	GAC	CTT	CCA	CGG	AAG	CCT	GAG	TGAGTTGACT	GACTACAGCT				551	
His	Lys	Arg	Ser	Asp	Leu	Pro	Arg	Lys	Pro	Glu							
1150				1155													
ACAACGGGGCT	GATGTCAGCC	ACTGCGAACA	TCAACGACAA	GATCGGGAAC	GTTCTAGTTG												611
GAGAAGGGGT	GACTGTTCTC	AGTCTACCGA	CTTCATATGA	CCTTAGTTAT	GTGAGACTCG												671
GTGACCCCAT	CCCCGCAGCA	GGACTCGACC	CGAAGTTGAT	GGCCACGTGC	GACAGTAGTG												731
ACAGACCCAG	AGTCTACACC	ATAACAGCTG	CAGATGAATA	CCAATTCTCG	TCACAACTCA												791
TCCCGAGTGG	CGTGAAGACC	ACACTGTTCT	CCGCCAACAT	CGATGCTCTC	ACCAGCTTCA												851
GCGTTGGTGG	TGAGCTTGTC	TTCAGCCAAG	TAACGATCCA	AAGCATTGAA	GTGGACGTCA												911
CCATTCACTT	CATTGGGTTT	GACGGGACAG	ACGTAGCAGT	CAAGGCAGTT	GCAACAGACT												971
TTGGGCTGAC	AACTGGGACA	AACAACCTTG	TGCCATTCAA	CCTGGTGGTC	CCAACAAATG												1031
AGATCACCCA	GCCCATCACT	TCCATGAAAC	TAGAGGTTGT	GACCTACAAG	ATTGGCGGCA												1091
CCGCTGGTGA	CCCAATATCA	TGGACAGTGA	GTGGTACACT	AGCTGTGACG	GTGCACGGAG												1151
GCAACTACCC	TGGGGCTCTC	CGTCCTGTCA	CCCTGGTGGC	CTATGAACGA	GTGGCTGCAG												1211
GATCTGTTGT	CACAGTTGCA	GGGGTGAGCA	ACTTCGAGCT	AATCCCCAAC	CCTGAGCTTG												1271
CAAAGAACCT	AGTTACAGAG	TATGGCCGCT	TTGACCCCGG	AGCAATGAAC	TACACCAAAC												1331
TAATACTGAG	TGAGAGAGAT	CGTCTAGGCA	TCAAGACAGT	CTGGCCCCACC	AGGGAGTACA												1391
CCGATTTTCA	GGAGTACTTC	ATGGAGGTTG	CAGATCTCAA	CTCACCCCTA	AAGATTGCAG												1451

GAGCATTTGG CTTTAAGGAC ATAATCCGAG CCATTCGGAA GATTGCGGTG CCAGTGGTAT 1511  
CCACACTCTT CCCTCCAGCT GCACCCCTAG CACATGCAAT CGGAGAAGGT GTAGACTACC 1571  
TCCTGGGCGA CGAGGCCCAA GCAGCCTCAG GGACAGCTCG AGCCGCGTCA GGAAAAGCTA 1631  
GAGCTGCCTC AGGACGAATA AGGCAGCTAA CTCTCGCAGC TGACAAGGGG TGCAGGGTAG 1691  
TCGCCAACAT GTTCCAGGTG CCCCAGAATC CCATTGTTGA TGGCATTCTG GCATCCCCAG 1751  
GAATCCTGCG TGGCGCACAC AACCTCGACT GCGTGCTATG GGAGGGAGCC ACTCTTTTCC 1811  
CTGTTGTCAT TACGACACTC GAGGATGAGC TGACCCCCAA GGCCTGAAC AGCAAAATGT 1871  
TTGCTGTCAT TGAAGGTGTG CGAGAGGACC TCCAGCCTCC ATCCCAACGG GGATCCTTCA 1931  
TTCGAACTCT CTCTGGCCAT AGAGTCTATG GCTATGCCCC AGACGGAGTA CTGCCTCTGG 1991  
AGACCGGGAG AGACTACACC GTTGTCCCAA TTGATGATGT GTGGGACGAT AGCATAATGC 2051  
TGTCGCAGGA CCCCATACCT CCAATCATAG GGAACAGCGG CAACCTAGCC ATAGCATACA 2111  
TGGATGTCTT CAGGCCCAAG GTCCCCATCC ACGTGGCTAT GACAGGGGCC CTCAATGCCC 2171  
GCGGTGAGAT CGAGAGTGTT ACGTTCCGCA GCACCAAACCT CGCCACAGCC CACCGACTTG 2231  
GCATGAAGTT AGCTGGTCCT GGAGCCTATG ACATTAATAC AGGACCTAAC TGGGCAACGT 2291  
TCGTCAAACG TTTCCCTCAC AATCCCCGAG ACTGGGACAG GTTGCCCTAC CTCAACCTTC 2351  
CTTATCTCCC ACCAACAGCA GGACGTCAGT TCCATCTAGC CCTGGCTGCC TCCGAGTTCA 2411  
AAGAGACCCC AGAACTCGAA GACGCTGTGC GCGCAATGGA TGCCGCTGCA AATGCCGACC 2471  
CATTGTTCCG CTCAGCTCTC CAGGTCTTCA TGTGGTTGGA AGAAAACGGG ATTGTGACCG 2531  
ACATGGCTAA CTTCGCCCTC AGCGACCCAA ACGCGCATAG GATGAAAAAC TTCCTAGCAA 2591  
ACGCACCCCA GGCTGGAAGC AAGTCGCAGA GGGCCAAGTA TGGCACGGCA GGCTACGGAG 2651  
TGGAGGCTCG AGGCCCCACA CCAGAAGAGG CACAGAGGGA AAAAGACACA CGGATCTCCA 2711  
AGAAGATGGA AACAATGGGC ATCTACTTCG CGACACCGGA ATGGGTGGCT CTCAACGGGC 2771  
ACCGAGGCCC AAGCCCCGGC CAACTCAAGT ACTGGCAAAA CACAAGAGAA ATACCAGAGC 2831  
CCAATGAGGA CTACCCAGAC TATGTGCACG CGGAGAAGAG CCGGTTGGCG TCAGAAGAAC 2891  
AGATCCTACG GGCAGCCACG TCGATCTACG GGGCTCCAGG ACAGGCTGAA CCACCCAGG 2951  
CCTTCATAGA CGAGGTCGCC AGGGTCTATG AAATCAACCA TGGGCGTGGT CCAAACCAGG 3011

AGCAGATGAA GGACCTGCTC CTGACTGCGA TGGAGATGAA GCATCGCAAT CCCAGGCGGG 3071  
 CTCCACCAAA GCCAAAGCCA AAACCCAATG CTCCATCACA GAGACCCCCT GGACGGCTGG 3131  
 GCCGCTGGAT CAGGACGGTC TCCGACGAGG ACTTGGAGTG AGGCTCCTGG GAGTCTCCCG 3191  
 ACACTACCCG CGCAGGTGTG GACACCAATT CGGCCTTCTA CCATCCCAA TTGGATCCGT 3251  
 TCGCGGGTCC CCT 3264

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met	Val	Ser	Arg	Asp	Gln	Thr	Asn	Asp	Arg	Ser	Asp	Asp	Lys	Pro	Asp	1	5	10	15
Gly	Ser	His	Pro	Thr	Asp	Cys	Ser	Val	His	Thr	Glu	Pro	Ser	Asp	Ala	20	25	30	
Asn	Asp	Arg	Thr	Gly	Val	His	Ser	Gly	Arg	His	Pro	Gly	Glu	Ala	His	35	40	45	
Thr	Gln	Val	Arg	Asn	Leu	Asp	Leu	Gln	Leu	Asp	Cys	Arg	Gly	Tyr	Arg	50	55	60	
Val	Arg	Thr	Asn	Cys	Leu	Phe	Pro	Trp	Ile	Pro	Trp	Phe	Ser	Cys	Arg	65	70	75	80
Cys	Ser	Leu	His	Thr	Ala	Glu	Gln	Trp	Glu	Leu	Pro	Ile	Arg	Pro	Asp	85	90	95	
Ala	Pro	Asp	Ser	Ala	Glu	Pro	Ala	Cys	Gln	Leu	Gln	Leu	Leu	Gln	Ala	100	105	110	
Ser	Glu	Gln	Glu	Ser	Asn	Arg	Thr	Val	Lys	His	Thr	Pro	Trp	Trp	Arg	115	120	125	
Leu	Cys	Thr	Lys	Arg	Asn	His	Lys	Arg	Ser	Asp	Leu	Pro	Arg	Lys	Pro	130	135	140	
Glu																145			

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 131..3169

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```

GGATACGATC GGTCTGACCC CGGGGGAGTC ACCCGGGGAC AGGCCATCAC TGCCTTGTTTC      60
CTGTTGGAA CTCCTCTTTC TGCTGTACTA TCGTTGATGG TGAGTAGAGA TCAGACAAAC      120
GATCGCAGCG ATG ACA AAC CTG ATG GAT CAC ACC CAA CAG ATT GTT CCG      169
      Met Thr Asn Leu Met Asp His Thr Gln Gln Ile Val Pro
                                150                                155

TTC ATA CGG AGC CTT CTG ATG CCA ACG ACC GGA CCG GCG TCC ATT CCG      217
Phe Ile Arg Ser Leu Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro
      160                                165                                170

GAC GAC ACC CTG GAG AAG CAC ACA CTC AGG TCC GAA ACC TCG ACT TAC      265
Asp Asp Thr Leu Glu Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr
      175                                180                                185                                190

AAC TTG ACT GTA GGG GAT ACA GGG TCA GGA CTA ATT GTC TTT TTC CCT      313
Asn Leu Thr Val Gly Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro
                                195                                200                                205

GGA TTC CCT GGT TCA GTT GTA GGT GCT CAC TAC ACA CTG CAG AGC AGT      361
Gly Phe Pro Gly Ser Val Val Gly Ala His Tyr Thr Leu Gln Ser Ser
                                210                                215                                220

GGG AAC TAC CAA TTC GAC CAG ATG CTC CTG ACA GCG CAG AAC CTG CCT      409
Gly Asn Tyr Gln Phe Asp Gln Met Leu Leu Thr Ala Gln Asn Leu Pro
                                225                                230                                235

GCC AGC TAC AAC TAC TGC AGG CTA GTG AGC AGG AGT CTA ACC GTA CGG      457
Ala Ser Tyr Asn Tyr Cys Arg Leu Val Ser Arg Ser Leu Thr Val Arg
      240                                245                                250

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## 55

TCA	AGC	ACA	CTC	CCT	GGT	GGC	GTT	TAT	GCA	CTA	AAC	GGA	ACC	ATA	AAC	505
Ser	Ser	Thr	Leu	Pro	Gly	Gly	Val	Tyr	Ala	Leu	Asn	Gly	Thr	Ile	Asn	
255					260					265					270	
GCA	GTG	ACC	TTC	CAC	GGA	AGC	CTG	AGT	GAG	TTG	ACT	GAC	TAC	AGC	TAC	553
Ala	Val	Thr	Phe	His	Gly	Ser	Leu	Ser	Glu	Leu	Thr	Asp	Tyr	Ser	Tyr	
				275					280						285	
AAC	GGG	CTG	ATG	TCA	GCC	ACT	GCG	AAC	ATC	AAC	GAC	AAG	ATC	GGG	AAC	601
Asn	Gly	Leu	Met	Ser	Ala	Thr	Ala	Asn	Ile	Asn	Asp	Lys	Ile	Gly	Asn	
			290					295					300			
GTT	CTA	GTT	GGA	GAA	GGG	GTG	ACT	GTT	CTC	AGT	CTA	CCG	ACT	TCA	TAT	649
Val	Leu	Val	Gly	Glu	Gly	Val	Thr	Val	Leu	Ser	Leu	Pro	Thr	Ser	Tyr	
		305					310					315				
GAC	CTT	AGT	TAT	GTG	AGA	CTC	GGT	GAC	CCC	ATC	CCC	GCA	GCA	GGA	CTC	697
Asp	Leu	Ser	Tyr	Val	Arg	Leu	Gly	Asp	Pro	Ile	Pro	Ala	Ala	Gly	Leu	
	320					325					330					
GAC	CCG	AAG	TTG	ATG	GCC	ACG	TGC	GAC	AGT	AGT	GAC	AGA	CCC	AGA	GTC	745
Asp	Pro	Lys	Leu	Met	Ala	Thr	Cys	Asp	Ser	Ser	Asp	Arg	Pro	Arg	Val	
335					340				345						350	
TAC	ACC	ATA	ACA	GCT	GCA	GAT	GAA	TAC	CAA	TTC	TCG	TCA	CAA	CTC	ATC	793
Tyr	Thr	Ile	Thr	Ala	Ala	Asp	Glu	Tyr	Gln	Phe	Ser	Ser	Gln	Leu	Ile	
				355					360					365		
CCG	AGT	GGC	GTG	AAG	ACC	ACA	CTG	TTC	TCC	GCC	AAC	ATC	GAT	GCT	CTC	841
Pro	Ser	Gly	Val	Lys	Thr	Thr	Leu	Phe	Ser	Ala	Asn	Ile	Asp	Ala	Leu	
			370					375					380			
ACC	AGC	TTC	AGC	GTT	GGT	GGT	GAG	CTT	GTC	TTC	AGC	CAA	GTA	ACG	ATC	889
Thr	Ser	Phe	Ser	Val	Gly	Gly	Glu	Leu	Val	Phe	Ser	Gln	Val	Thr	Ile	
		385					390					395				
CAA	AGC	ATT	GAA	GTG	GAC	GTC	ACC	ATT	CAC	TTC	ATT	GGG	TTT	GAC	GGG	937
Gln	Ser	Ile	Glu	Val	Asp	Val	Thr	Ile	His	Phe	Ile	Gly	Phe	Asp	Gly	
	400					405					410					
ACA	GAC	GTA	GCA	GTC	AAG	GCA	GTT	GCA	ACA	GAC	TTT	GGG	CTG	ACA	ACT	985
Thr	Asp	Val	Ala	Val	Lys	Ala	Val	Ala	Thr	Asp	Phe	Gly	Leu	Thr	Thr	
415					420				425						430	
GGG	ACA	AAC	AAC	CTT	GTG	CCA	TTC	AAC	CTG	GTG	GTC	CCA	ACA	AAT	GAG	1033
Gly	Thr	Asn	Asn	Leu	Val	Pro	Phe	Asn	Leu	Val	Val	Pro	Thr	Asn	Glu	
				435					440					445		
ATC	ACC	CAG	CCC	ATC	ACT	TCC	ATG	AAA	CTA	GAG	GTT	GTG	ACC	TAC	AAG	1081
Ile	Thr	Gln	Pro	Ile	Thr	Ser	Met	Lys	Leu	Glu	Val	Val	Thr	Tyr	Lys	
			450					455					460			

ATT	GGC	GGC	ACC	GCT	GGT	GAC	CCA	ATA	TCA	TGG	ACA	GTG	AGT	GGT	ACA	1129
Ile	Gly	Gly	Thr	Ala	Gly	Asp	Pro	Ile	Ser	Trp	Thr	Val	Ser	Gly	Thr	
	465						470					475				
CTA	GCT	GTG	ACG	GTG	CAC	GGA	GGC	AAC	TAC	CCT	GGG	GCT	CTC	CGT	CCT	1177
Leu	Ala	Val	Thr	Val	His	Gly	Gly	Asn	Tyr	Pro	Gly	Ala	Leu	Arg	Pro	
	480					485					490					
GTC	ACC	CTG	GTG	GCC	TAT	GAA	CGA	GTG	GCT	GCA	GGA	TCT	GTT	GTC	ACA	1225
Val	Thr	Leu	Val	Ala	Tyr	Glu	Arg	Val	Ala	Ala	Gly	Ser	Val	Val	Thr	
495					500					505					510	
GTT	GCA	GGG	GTG	AGC	AAC	TTC	GAG	CTA	ATC	CCC	AAC	CCT	GAG	CTT	GCA	1273
Val	Ala	Gly	Val	Ser	Asn	Phe	Glu	Leu	Ile	Pro	Asn	Pro	Glu	Leu	Ala	
				515					520					525		
AAG	AAC	CTA	GTT	ACA	GAG	TAT	GGC	CGC	TTT	GAC	CCC	GGA	GCA	ATG	AAC	1321
Lys	Asn	Leu	Val	Thr	Glu	Tyr	Gly	Arg	Phe	Asp	Pro	Gly	Ala	Met	Asn	
		530						535					540			
TAC	ACC	AAA	CTA	ATA	CTG	AGT	GAG	AGA	GAT	CGT	CTA	GGC	ATC	AAG	ACA	1369
Tyr	Thr	Lys	Leu	Ile	Leu	Ser	Glu	Arg	Asp	Arg	Leu	Gly	Ile	Lys	Thr	
		545					550					555				
GTC	TGG	CCC	ACC	AGG	GAG	TAC	ACC	GAT	TTC	AGG	GAG	TAC	TTC	ATG	GAG	1417
Val	Trp	Pro	Thr	Arg	Glu	Tyr	Thr	Asp	Phe	Arg	Glu	Tyr	Phe	Met	Glu	
	560					565					570					
GTT	GCA	GAT	CTC	AAC	TCA	CCC	CTA	AAG	ATT	GCA	GGA	GCA	TTT	GGC	TTT	1465
Val	Ala	Asp	Leu	Asn	Ser	Pro	Leu	Lys	Ile	Ala	Gly	Ala	Phe	Gly	Phe	
575					580					585					590	
AAG	GAC	ATA	ATC	CGA	GCC	ATT	CGG	AAG	ATT	GCG	GTG	CCA	GTG	GTA	TCC	1513
Lys	Asp	Ile	Ile	Arg	Ala	Ile	Arg	Lys	Ile	Ala	Val	Pro	Val	Val	Ser	
				595					600					605		
ACA	CTC	TTC	CCT	CCA	GCT	GCA	CCC	CTA	GCA	CAT	GCA	ATC	GGA	GAA	GGT	1561
Thr	Leu	Phe	Pro	Pro	Ala	Ala	Pro	Leu	Ala	His	Ala	Ile	Gly	Glu	Gly	
			610					615					620			
GTA	GAC	TAC	CTC	CTG	GGC	GAC	GAG	GCC	CAA	GCA	GCC	TCA	GGG	ACA	GCT	1609
Val	Asp	Tyr	Leu	Leu	Gly	Asp	Glu	Ala	Gln	Ala	Ala	Ser	Gly	Thr	Ala	
		625					630					635				
CGA	GCC	GCG	TCA	GGA	AAA	GCT	AGA	GCT	GCC	TCA	GGA	CGA	ATA	AGG	CAG	1657
Arg	Ala	Ala	Ser	Gly	Lys	Ala	Arg	Ala	Ala	Ser	Gly	Arg	Ile	Arg	Gln	
	640					645					650					
CTA	ACT	CTC	GCA	GCT	GAC	AAG	GGG	TGC	GAG	GTA	GTC	GCC	AAC	ATG	TTC	1705
Leu	Thr	Leu	Ala	Ala	Asp	Lys	Gly	Cys	Glu	Val	Val	Ala	Asn	Met	Phe	
655					660				665						670	

CAG	GTG	CCC	CAG	AAT	CCC	ATT	GTT	GAT	GGC	ATT	CTG	GCA	TCC	CCA	GGA	1753
Gln	Val	Pro	Gln	Asn	Pro	Ile	Val	Asp	Gly	Ile	Leu	Ala	Ser	Pro	Gly	
				675					680						685	
ATC	CTG	CGT	GGC	GCA	CAC	AAC	CTC	GAC	TGC	GTG	CTA	TGG	GAG	GGA	GCC	1801
Ile	Leu	Arg	Gly	Ala	His	Asn	Leu	Asp	Cys	Val	Leu	Trp	Glu	Gly	Ala	
			690					695					700			
ACT	CTT	TTC	CCT	GTT	GTC	ATT	ACG	ACA	CTC	GAG	GAT	GAG	CTG	ACC	CCC	1849
Thr	Leu	Phe	Pro	Val	Val	Ile	Thr	Thr	Leu	Glu	Asp	Glu	Leu	Thr	Pro	
		705					710					715				
AAG	GCA	CTG	AAC	AGC	AAA	ATG	TTT	GCT	GTC	ATT	GAA	GGT	GTG	CGA	GAG	1897
Lys	Ala	Leu	Asn	Ser	Lys	Met	Phe	Ala	Val	Ile	Glu	Gly	Val	Arg	Glu	
	720					725					730					
GAC	CTC	CAG	CCT	CCA	TCC	CAA	CGG	GGA	TCC	TTC	ATT	CGA	ACT	CTC	TCT	1945
Asp	Leu	Gln	Pro	Pro	Ser	Gln	Arg	Gly	Ser	Phe	Ile	Arg	Thr	Leu	Ser	
735					740					745					750	
GGC	CAT	AGA	GTC	TAT	GGC	TAT	GCC	CCA	GAC	GGA	GTA	CTG	CCT	CTG	GAG	1993
Gly	His	Arg	Val	Tyr	Gly	Tyr	Ala	Pro	Asp	Gly	Val	Leu	Pro	Leu	Glu	
			755					760					765			
ACC	GGG	AGA	GAC	TAC	ACC	GTT	GTC	CCA	ATT	GAT	GAT	GTG	TGG	GAC	GAT	2041
Thr	Gly	Arg	Asp	Tyr	Thr	Val	Val	Pro	Ile	Asp	Asp	Val	Trp	Asp	Asp	
			770					775					780			
AGC	ATA	ATG	CTG	TCG	CAG	GAC	CCC	ATA	CCT	CCA	ATC	ATA	GGG	AAC	AGC	2089
Ser	Ile	Met	Leu	Ser	Gln	Asp	Pro	Ile	Pro	Pro	Ile	Ile	Gly	Asn	Ser	
	785						790					795				
GGC	AAC	CTA	GCC	ATA	GCA	TAC	ATG	GAT	GTC	TTC	AGG	CCC	AAG	GTC	CCC	2137
Gly	Asn	Leu	Ala	Ile	Ala	Tyr	Met	Asp	Val	Phe	Arg	Pro	Lys	Val	Pro	
	800					805					810					
ATC	CAC	GTG	GCT	ATG	ACA	GGG	GCC	CTC	AAT	GCC	CGC	GGT	GAG	ATC	GAG	2185
Ile	His	Val	Ala	Met	Thr	Gly	Ala	Leu	Asn	Ala	Arg	Gly	Glu	Ile	Glu	
815					820					825					830	
AGT	GTT	ACG	TTC	CGC	AGC	ACC	AAA	CTC	GCC	ACA	GCC	CAC	CGA	CTT	GGC	2233
Ser	Val	Thr	Phe	Arg	Ser	Thr	Lys	Leu	Ala	Thr	Ala	His	Arg	Leu	Gly	
				835					840					845		
ATG	AAG	TTA	GCT	GGT	CCT	GGA	GCC	TAT	GAC	ATT	AAT	ACA	GGA	CCT	AAC	2281
Met	Lys	Leu	Ala	Gly	Pro	Gly	Ala	Tyr	Asp	Ile	Asn	Thr	Gly	Pro	Asn	
			850					855					860			
TGG	GCA	ACG	TTC	GTC	AAA	CGT	TTC	CCT	CAC	AAT	CCC	CGA	GAC	TGG	GAC	2329
Trp	Ala	Thr	Phe	Val	Lys	Arg	Phe	Pro	His	Asn	Pro	Arg	Asp	Trp	Asp	
			865				870					875				

AGG	TTG	CCC	TAC	CTC	AAC	CTT	CCT	TAT	CTC	CCA	CCA	ACA	GCA	GGA	CGT	2377
Arg	Leu	Pro	Tyr	Leu	Asn	Leu	Pro	Tyr	Leu	Pro	Pro	Thr	Ala	Gly	Arg	
880						885					890					
CAG	TTC	CAT	CTA	GCC	CTG	GCT	GCC	TCC	GAG	TTC	AAA	GAG	ACC	CCA	GAA	2425
Gln	Phe	His	Leu	Ala	Leu	Ala	Ala	Ser	Glu	Phe	Lys	Glu	Thr	Pro	Glu	
895					900				905						910	
CTC	GAA	GAC	GCT	GTG	CGC	GCA	ATG	GAT	GCC	GCT	GCA	AAT	GCC	GAC	CCA	2473
Leu	Glu	Asp	Ala	Val	Arg	Ala	Met	Asp	Ala	Ala	Ala	Asn	Ala	Asp	Pro	
				915					920					925		
TTG	TTC	CGC	TCA	GCT	CTC	CAG	GTC	TTC	ATG	TGG	TTG	GAA	GAA	AAC	GGG	2521
Leu	Phe	Arg	Ser	Ala	Leu	Gln	Val	Phe	Met	Trp	Leu	Glu	Glu	Asn	Gly	
			930					935						940		
ATT	GTG	ACC	GAC	ATG	GCT	AAC	TTC	GCC	CTC	AGC	GAC	CCA	AAC	GCG	CAT	2569
Ile	Val	Thr	Asp	Met	Ala	Asn	Phe	Ala	Leu	Ser	Asp	Pro	Asn	Ala	His	
		945					950					955				
AGG	ATG	AAA	AAC	TTC	CTA	GCA	AAC	GCA	CCC	CAG	GCT	GGA	AGC	AAG	TCG	2617
Arg	Met	Lys	Asn	Phe	Leu	Ala	Asn	Ala	Pro	Gln	Ala	Gly	Ser	Lys	Ser	
	960					965					970					
CAG	AGG	GCC	AAG	TAT	GGC	ACG	GCA	GGC	TAC	GGA	GTG	GAG	GCT	CGA	GGC	2665
Gln	Arg	Ala	Lys	Tyr	Gly	Thr	Ala	Gly	Tyr	Gly	Val	Glu	Ala	Arg	Gly	
975					980					985					990	
CCC	ACA	CCA	GAA	GAG	GCA	CAG	AGG	GAA	AAA	GAC	ACA	CGG	ATC	TCC	AAG	2713
Pro	Thr	Pro	Glu	Glu	Ala	Gln	Arg	Glu	Lys	Asp	Thr	Arg	Ile	Ser	Lys	
				995					1000					1005		
AAG	ATG	GAA	ACA	ATG	GGC	ATC	TAC	TTC	GCG	ACA	CCG	GAA	TGG	GTG	GCT	2761
Lys	Met	Glu	Thr	Met	Gly	Ile	Tyr	Phe	Ala	Thr	Pro	Glu	Trp	Val	Ala	
			1010					1015					1020			
CTC	AAC	GGG	CAC	CGA	GGC	CCA	AGC	CCC	GGC	CAA	CTC	AAG	TAC	TGG	CAA	2809
Leu	Asn	Gly	His	Arg	Gly	Pro	Ser	Pro	Gly	Gln	Leu	Lys	Tyr	Trp	Gln	
			1025				1030						1035			
AAC	ACA	AGA	GAA	ATA	CCA	GAG	CCC	AAT	GAG	GAC	TAC	CCA	GAC	TAT	GTG	2857
Asn	Thr	Arg	Glu	Ile	Pro	Glu	Pro	Asn	Glu	Asp	Tyr	Pro	Asp	Tyr	Val	
	1040					1045					1050					
CAC	GCG	GAG	AAG	AGC	CGG	TTG	GCG	TCA	GAA	GAA	CAG	ATC	CTA	CGG	GCA	2905
His	Ala	Glu	Lys	Ser	Arg	Leu	Ala	Ser	Glu	Glu	Gln	Ile	Leu	Arg	Ala	
1055					1060					1065					1070	
GCC	ACG	TCG	ATC	TAC	GGG	GCT	CCA	GGA	CAG	GCT	GAA	CCA	CCC	CAG	GCC	2953
Ala	Thr	Ser	Ile	Tyr	Gly	Ala	Pro	Gly	Gln	Ala	Glu	Pro	Pro	Gln	Ala	
				1075					1080					1085		

TTC ATA GAC GAG GTC GCC AGG GTC TAT GAA ATC AAC CAT GGG CGT GGT 3001  
 Phe Ile Asp Glu Val Ala Arg Val Tyr Glu Ile Asn His Gly Arg Gly  
                   1090                  1095                  1100

CCA AAC CAG GAG CAG ATG AAG GAC CTG CTC CTG ACT GCG ATG GAG ATG 3049  
 Pro Asn Gln Glu Gln Met Lys Asp Leu Leu Leu Thr Ala Met Glu Met  
                   1105                  1110                  1115

AAG CAT CGC AAT CCC AGG CGG GCT CCA CCA AAG CCA AAG CCA AAA CCC 3097  
 Lys His Arg Asn Pro Arg Arg Ala Pro Pro Lys Pro Lys Pro Lys Pro  
                   1120                  1125                  1130

AAT GCT CCA TCA CAG AGA CCC CCT GGA CGG CTG GGC CGC TGG ATC AGG 3145  
 Asn Ala Pro Ser Gln Arg Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg  
                   1135                  1140                  1145                  1150

ACG GTC TCC GAC GAG GAC TTG GAG TGAGGCTCCT GGGAGTCTCC CGACACTACC 3199  
 Thr Val Ser Asp Glu Asp Leu Glu  
                   1155

CGCGCAGGTG TGGACACCAA TTCGGCCTTC TACCATCCCA AATTGGATCC GTTCGCGGGT 3259

CCCCT 3264

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1013 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Thr Asn Leu Met Asp His Thr Gln Gln Ile Val Pro Phe Ile Arg  
   1                  5                  10                  15

Ser Leu Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro Asp Asp Thr  
                   20                  25                  30

Leu Glu Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr Asn Leu Thr  
                   35                  40                  45

Val Gly Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro Gly Phe Pro  
                   50                  55                  60

Gly Ser Val Val Gly Ala His Tyr Thr Leu Gln Ser Ser Gly Asn Tyr  
   65                  70                  75                  80

Gln Phe Asp Gln Met Leu Leu Thr Ala Gln Asn Leu Pro Ala Ser Tyr

60

	85		90		95
Asn Tyr Cys Arg Leu Val Ser Arg Ser Leu Thr Val Arg Ser Ser Thr	100		105		110
Leu Pro Gly Gly Val Tyr Ala Leu Asn Gly Thr Ile Asn Ala Val Thr	115		120		125
Phe His Gly Ser Leu Ser Glu Leu Thr Asp Tyr Ser Tyr Asn Gly Leu	130		135		140
Met Ser Ala Thr Ala Asn Ile Asn Asp Lys Ile Gly Asn Val Leu Val	145		150		155
					160
Gly Glu Gly Val Thr Val Leu Ser Leu Pro Thr Ser Tyr Asp Leu Ser	165		170		175
Tyr Val Arg Leu Gly Asp Pro Ile Pro Ala Ala Gly Leu Asp Pro Lys	180		185		190
Leu Met Ala Thr Cys Asp Ser Ser Asp Arg Pro Arg Val Tyr Thr Ile	195		200		205
Thr Ala Ala Asp Glu Tyr Gln Phe Ser Ser Gln Leu Ile Pro Ser Gly	210		215		220
Val Lys Thr Thr Leu Phe Ser Ala Asn Ile Asp Ala Leu Thr Ser Phe	225		230		235
					240
Ser Val Gly Gly Glu Leu Val Phe Ser Gln Val Thr Ile Gln Ser Ile	245		250		255
Glu Val Asp Val Thr Ile His Phe Ile Gly Phe Asp Gly Thr Asp Val	260		265		270
Ala Val Lys Ala Val Ala Thr Asp Phe Gly Leu Thr Thr Gly Thr Asn	275		280		285
Asn Leu Val Pro Phe Asn Leu Val Val Pro Thr Asn Glu Ile Thr Gln	290		295		300
Pro Ile Thr Ser Met Lys Leu Glu Val Val Thr Tyr Lys Ile Gly Gly	305		310		315
					320
Thr Ala Gly Asp Pro Ile Ser Trp Thr Val Ser Gly Thr Leu Ala Val	325		330		335
Thr Val His Gly Gly Asn Tyr Pro Gly Ala Leu Arg Pro Val Thr Leu	340		345		350
Val Ala Tyr Glu Arg Val Ala Ala Gly Ser Val Val Thr Val Ala Gly	355		360		365

Val	Ser	Asn	Phe	Glu	Leu	Ile	Pro	Asn	Pro	Glu	Leu	Ala	Lys	Asn	Leu	370	375	380	
Val	Thr	Glu	Tyr	Gly	Arg	Phe	Asp	Pro	Gly	Ala	Met	Asn	Tyr	Thr	Lys	385	390	395	400
Leu	Ile	Leu	Ser	Glu	Arg	Asp	Arg	Leu	Gly	Ile	Lys	Thr	Val	Trp	Pro	405	410	415	
Thr	Arg	Glu	Tyr	Thr	Asp	Phe	Arg	Glu	Tyr	Phe	Met	Glu	Val	Ala	Asp	420	425	430	
Leu	Asn	Ser	Pro	Leu	Lys	Ile	Ala	Gly	Ala	Phe	Gly	Phe	Lys	Asp	Ile	435	440	445	
Ile	Arg	Ala	Ile	Arg	Lys	Ile	Ala	Val	Pro	Val	Val	Ser	Thr	Leu	Phe	450	455	460	
Pro	Pro	Ala	Ala	Pro	Leu	Ala	His	Ala	Ile	Gly	Glu	Gly	Val	Asp	Tyr	465	470	475	480
Leu	Leu	Gly	Asp	Glu	Ala	Gln	Ala	Ala	Ser	Gly	Thr	Ala	Arg	Ala	Ala	485	490	495	
Ser	Gly	Lys	Ala	Arg	Ala	Ala	Ser	Gly	Arg	Ile	Arg	Gln	Leu	Thr	Leu	500	505	510	
Ala	Ala	Asp	Lys	Gly	Cys	Glu	Val	Val	Ala	Asn	Met	Phe	Gln	Val	Pro	515	520	525	
Gln	Asn	Pro	Ile	Val	Asp	Gly	Ile	Leu	Ala	Ser	Pro	Gly	Ile	Leu	Arg	530	535	540	
Gly	Ala	His	Asn	Leu	Asp	Cys	Val	Leu	Trp	Glu	Gly	Ala	Thr	Leu	Phe	545	550	555	560
Pro	Val	Val	Ile	Thr	Thr	Leu	Glu	Asp	Glu	Leu	Thr	Pro	Lys	Ala	Leu	565	570	575	
Asn	Ser	Lys	Met	Phe	Ala	Val	Ile	Glu	Gly	Val	Arg	Glu	Asp	Leu	Gln	580	585	590	
Pro	Pro	Ser	Gln	Arg	Gly	Ser	Phe	Ile	Arg	Thr	Leu	Ser	Gly	His	Arg	595	600	605	
Val	Tyr	Gly	Tyr	Ala	Pro	Asp	Gly	Val	Leu	Pro	Leu	Glu	Thr	Gly	Arg	610	615	620	
Asp	Tyr	Thr	Val	Val	Pro	Ile	Asp	Asp	Val	Trp	Asp	Asp	Ser	Ile	Met	625	630	635	640

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Leu Ser Gln Asp Pro Ile Pro Pro Ile Ile Gly Asn Ser Gly Asn Leu  
 645 650 655  
 Ala Ile Ala Tyr Met Asp Val Phe Arg Pro Lys Val Pro Ile His Val  
 660 665 670  
 Ala Met Thr Gly Ala Leu Asn Ala Arg Gly Glu Ile Glu Ser Val Thr  
 675 680 685  
 Phe Arg Ser Thr Lys Leu Ala Thr Ala His Arg Leu Gly Met Lys Leu  
 690 695 700  
 Ala Gly Pro Gly Ala Tyr Asp Ile Asn Thr Gly Pro Asn Trp Ala Thr  
 705 710 715 720  
 Phe Val Lys Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg Leu Pro  
 725 730 735  
 Tyr Leu Asn Leu Pro Tyr Leu Pro Pro Thr Ala Gly Arg Gln Phe His  
 740 745 750  
 Leu Ala Leu Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu Glu Asp  
 755 760 765  
 Ala Val Arg Ala Met Asp Ala Ala Ala Asn Ala Asp Pro Leu Phe Arg  
 770 775 780  
 Ser Ala Leu Gln Val Phe Met Trp Leu Glu Glu Asn Gly Ile Val Thr  
 785 790 795 800  
 Asp Met Ala Asn Phe Ala Leu Ser Asp Pro Asn Ala His Arg Met Lys  
 805 810 815  
 Asn Phe Leu Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala  
 820 825 830  
 Lys Tyr Gly Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro  
 835 840 845  
 Glu Glu Ala Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu  
 850 855 860  
 Thr Met Gly Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly  
 865 870 875 880  
 His Arg Gly Pro Ser Pro Gly Gln Leu Lys Tyr Trp Gln Asn Thr Arg  
 885 890 895  
 Glu Ile Pro Glu Pro Asn Glu Asp Tyr Pro Asp Tyr Val His Ala Glu  
 900 905 910



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Lys Ser Arg Leu Ala Ser Glu Glu Gln Ile Leu Arg Ala Ala Thr Ser  
915 920 925

Ile Tyr Gly Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp  
930 935 940

Glu Val Ala Arg Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln  
945 950 955 960

Glu Gln Met Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg  
965 970 975

Asn Pro Arg Arg Ala Pro Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro  
980 985 990

Ser Gln Arg Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Thr Val Ser  
995 1000 1005

Asp Glu Asp Leu Glu  
1010

## Claims

1. A method for preparing live Birnavirus, comprising the following steps:
  - preparing a cDNA containing infectious bursal disease virus genome segments A and B,
  - transcribing said cDNA to produce synthetic RNA transcripts,
  - transfecting host cells with said synthetic RNA transcripts,
  - incubating said host cells in a culture medium, and
  - isolating live infectious bursal disease virus from said culture medium.
2. The method according to claim 1, wherein said Birnavirus is infectious bursal disease virus.
3. The method according to claim 1, wherein said host cells are African green monkey Vero cells.
4. The method according to claim 1, wherein said segments A and B of said cDNA are independently prepared.
5. The method according to claim 4, wherein said segment A is present in plasmid pUC19FLAD78 or pUC18FLA23.
6. The method according to claim 4, wherein said segment B is present in plasmid pUC18FLBP2.
7. A live infectious bursal disease virus, wherein said virus is made by a process comprising the steps of preparing a cDNA containing infectious bursal disease virus genome segments A and B,
  - transcribing said cDNA to produce a synthetic RNA transcript,
  - transfecting a host cell with said synthetic RNA transcript,
  - incubating said host cell in a culture medium, and
  - isolating live infectious bursal disease virus from said culture medium.
8. A synthetic RNA encoding proteins VP1, VP2, VP3, VP4, and VP5 of infectious bursal disease virus.
9. A host cell transfected with the synthetic RNA according to claim 8.
10. A cDNA containing at least a portion of the infectious bursal disease virus genome selected from the group consisting of segment A,

segment B and segments A and B of infectious bursal disease virus, wherein said cDNA includes the 5' and 3' termini of said segments.

11. A recombinant vector comprising the cDNA according to claim 10.

12. The vector according to claim 11, wherein said vector is a plasmid.

13. The vector according to claim 12, wherein said plasmid is selected from the group consisting of pUC19FLAD78, pUC18FLA23 and pUC19FLBP2.

14. A host cell transformed with the vector according to claim 11.

15. A vaccine comprising an infectious bursal disease virus according to claim 7, wherein said infectious bursal disease virus is inactivated or attenuated prior to administration.

16. A method for producing a live infectious bursal disease virus vaccine, comprising the steps of

preparing a full-length cDNA containing infectious bursal disease virus genome segments A and B,

transcribing said cDNA to produce synthetic RNA transcripts,

purifying said synthetic RNA transcripts,

transfecting host cells with said purified RNA transcripts,

incubating said host cells in a culture medium,

isolating live infectious bursal disease virus from said culture medium,

attenuating said live infectious bursal disease virus to produce a virus with reduced virulence, and

combining said live infectious bursal disease virus with a pharmaceutically acceptable carrier to produce a live infectious bursal disease virus vaccine.

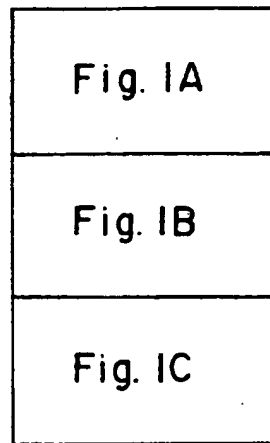
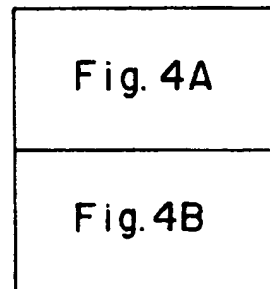
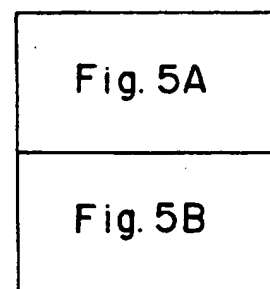
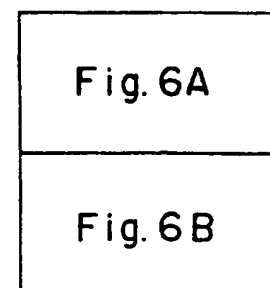
17. The method according to claim 16, wherein said live infectious bursal disease virus is attenuated by serial passage or site directed mutagenesis.

18. The method according to claim 1, wherein said host cells are poultry cells.

19. The method according to claim 18, wherein said poultry cells are chicken, turkey, or quail cells.

20. The method according to claim 19, wherein said poultry cells are chicken embryo fibroblast cells or chicken embryo kidney cells.

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**Fig. 1****Fig. 4****Fig. 5****Fig. 6**

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segment A of  
strain D78

pUC19FLAD78

SEQ ID No. 1

GAATTCGGCTTTAATACGACTCACTATAGGATACGATC66TCTGAC  
CTTAAGCCGAAATTATGCTGAGTGATA TCCTATGCTAGCCAGACTG

EcoR I

SEQ ID No. 2

AATTG6ATCCGTTTCGCGG6TCCCCT GTACAAAGCCGAATTC  
TTAACCTAGGCAAGC6CCCCA6666ACATG TTTG6GCTTAAG

BstG I

EcoR I

Transcription →

VP5

VP2-VP4-VP3

Fig.1A

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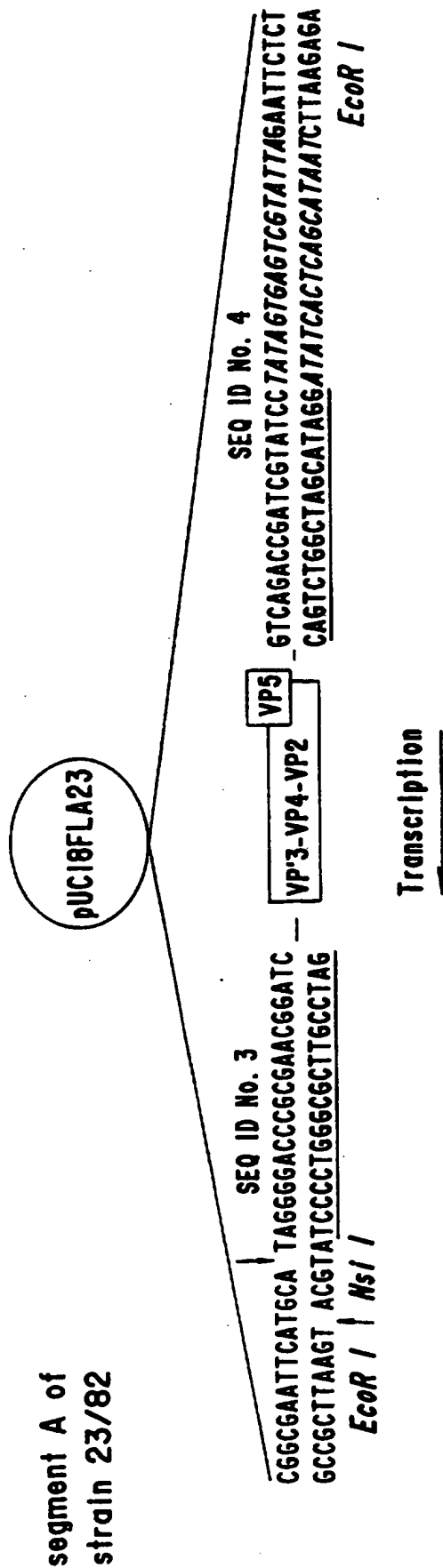


Fig.1B

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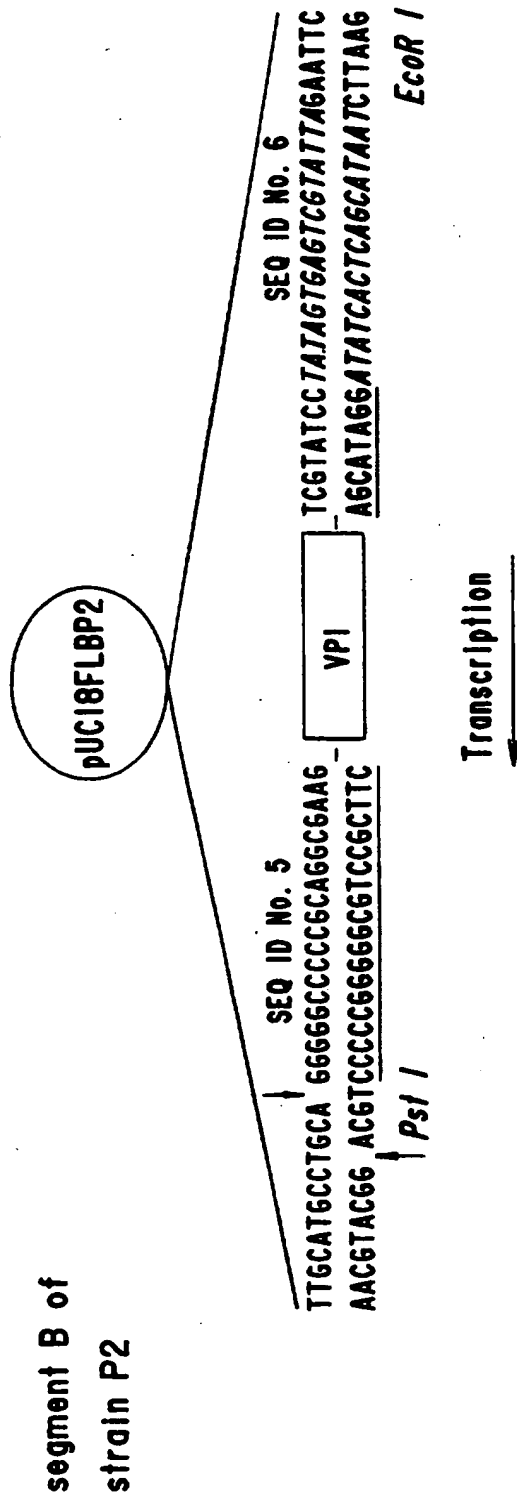


Fig.1C



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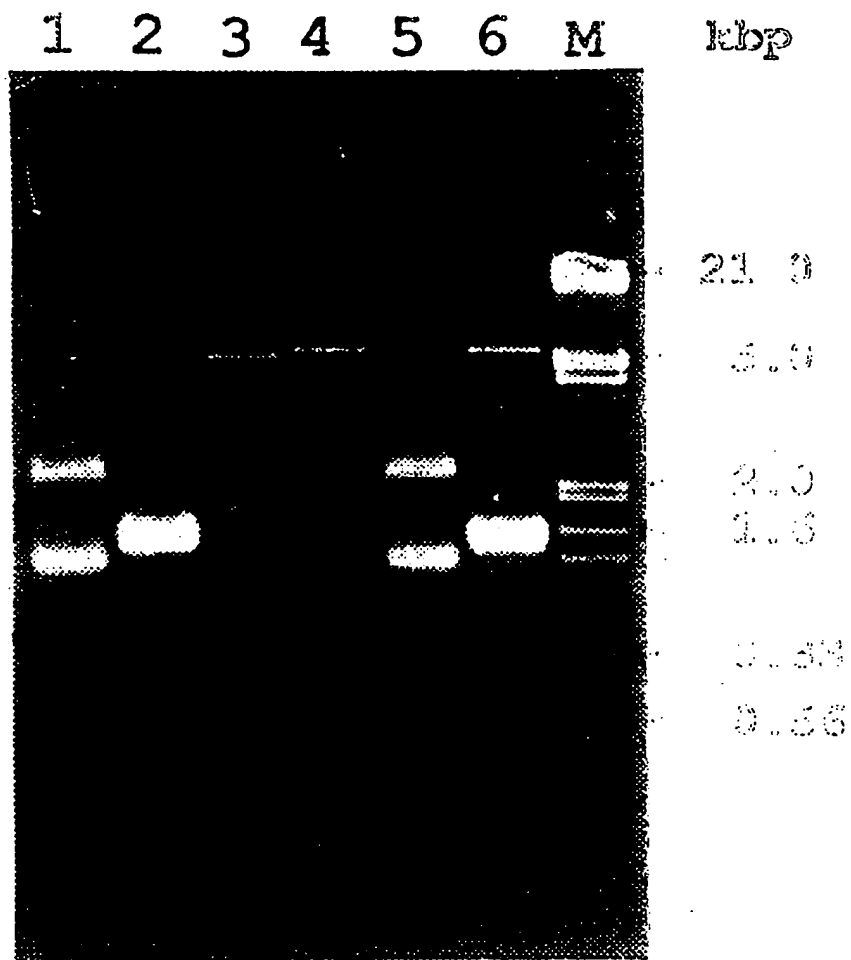


Fig. 2

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## Segment A

23-82A  
SEQ ID No. 723A/P2B  
SEQ ID No. 8P2A  
SEQ ID No. 9

530 540 550 560 570 580  
66AAGCCTGAGTGAGTTGACTGACTACAGCTACAACGGGCTGATGTCAGCCACTGCCGAAC  
.....  
66AAGCCTGAGTGAGTTGACTGACTACAGCTACAACGGGCTGATGTCAGCCACTGCCGAAC  
.....  
66AAGCCTGAGTGAGTTGACTGACTACAGCTACAACGGGCTGATGTCAGCCACTGCCGAAC  
530 540 550 560 570 580

23-82A  
SEQ ID No. 723A/P2B  
SEQ ID No. 8P2A  
SEQ ID No. 9

590 600 610 620 630 640  
ATCAACGACAAAGATCGGGAAACGTTCTAGTTGGAGAAAGGGGCTGACTGTTCTCAGTCTACCG  
.....  
ATCAACGACAAAGATCGGGAAACGTTCTAGTTGGAGAAAGGGGCTGACTGTTCTCAGTCTACCG  
.....  
ATCAACGACAAAGATCGGGAAACGTTCTAGTTGGAGAAAGGGGCTGACTGTTCTCAGTCTACCG  
590 600 610 620 630 640

Fig.3A

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## Segment B

23-82B	130	140	150	160	170	180
SEQ ID No. 10	TTTTCAATAGTCCACAGGCGGGAACGAAGATCTCAGCAGCGTTTCGGCATAAAGCCTACTG					
23A/P2B	TTTTCAACAGTCCACAGGCGGGAACGAAGATCTCAGCAGCGTTTCGGCATAAAGCCTACTG					
SEQ ID No. 11	TTTTCAACAGTCCACAGGCGGGAACGAAGATCTCAGCAGCGTTTCGGCATAAAGCCTACTG					
P2B	TTTTCAACAGTCCACAGGCGGGAACGAAGATCTCAGCAGCGTTTCGGCATAAAGCCTACTG					
SEQ ID No. 12	130	140	150	160	170	180
23-82B	190	200	210	220	230	240
SEQ ID No. 10	CTGGACAAGACGTGGAAAGAACTCTTGTATCCCAAGTCTGGGTGCCACCTGAGGATCCGC					
23A/P2B	CTGGACAAGACGTGGAAAGAACTCTTGTATCCCAAGTCTGGGTGCCACCTGAGGATCCGC					
SEQ ID No. 11	CTGGACAAGACGTGGAAAGAACTCTTGTATCCCAAGTCTGGGTGCCACCTGAGGATCCGC					
P2B	CTGGACAAGACGTGGAAAGAACTCTTGTATCCCAAGTCTGGGTGCCACCTGAGGATCCGC					
SEQ ID No. 12	190	200	210	220	230	240

Fig.3B

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Fig.4A

1 GGATACGATCGGTCGACCCCGGGGAGTCACCCGGGGACAGGCCATCACTGCCCTTGTTCCTGGTTGGAA  
 71 CTCCTCTTTCTGCTGTACTATCGTTGATGGTAGAGATCAGACAAACGATCGCAGCGATGACAAACC  
 141 TGATGGATCACACCCAAACAGATTGTTCCGTTTCATACGGAGCCTTCTGATGCCAACGACCGGACCGCGTC  
 211 CATTCCGGACGACACCCCTGGAGAAGCACACACTCAGGTCGGAACCTCGACTTACAACTTGACTGTAGGG  
 281 GATACAGGGTCAGGACTAATTGTCCTTTTCCCTGGATCCCTGGTTCCAGTTGAGGTGCTCACTACACAC  
 351 TGCAGAGCAGTGGAACTACCAATTCCAGCAGATGCTCTGACAGCGCAGAACCTGCCAGCTACAA  
 421 CTACTGCAGGCTAGTGAGCAGGAGTCAACCGTACGGTCAAGCACACTCCCTGGTGGGTTTATGCACTA  
 491 AACGGAACCATAAACGCAGTGACCTTCCACGGAAGCCTGAGTGAGTTGACTGACTACAGTACAACGGGC  
 561 TGATGTCAGCCACTGCGAACAATCAACGACAAGATCGGGAACGTTCTAGTTGGAGAAGGGTGACTGTTCT  
 631 CAGTCTACCGACTTCATATGACCTTAGTTATGTGAGACTCGGTGACCCCATCCCGCAGCAGGACTCGAC  
 701 CCGAAGTTGATGGCCACGTGCGACAGTAGTGACAGACCCAGAGTCTACACCATAACAGCTGCAGATGAAT  
 771 ACCAATTCTCGTCACAACCTCATCCCGAGTGGCGTGAAGACCACACTGTTCTCCGCCAACATCGATGCTCT  
 841 CACCAGCTTCAGCGTTGGTGGTGAGCTTGCTTCAGCCCAAGTAACGATCCAAAGCATTGAAGTGACGTC  
 911 ACCATTCACTTCAATTGGGTTTGACGGGACAGACGTAGCAGTCAAGGCAGTTGCAACAGACTTTGGGCTGA  
 981 CAACTGGGACAAACAACCTTGTCCTTCAACCTGGTGGTCCCAACAAATGAGATCACCCAGCCCATCAC  
 1051 TTCCATGAAACTAGAGGTTGTGACCTACAAGATTGGCGGCACCGCTGGTGACCCAAATATCATGGACAGTG  
 1121 AGTGGTACACTAGCTGTGACGGTGCACGGAGGCAACTACCTGGGGCTCTCCGTCTGTCAACCCTGGTGG  
 1191 CCTATGAACGAGTGGCTGCAGGATCTGTTGTACAGTTGCAGGGGTGAGCAACTTCGAGCTAATCCCCAA  
 1261 CCCTGAGCTTGCAAGAACCTAGTTACAGAGTATGGCCGCTTGACCCCGGAGCAATGAACATACACCAA  
 1331 CTAATACTGAGTGAGAGAGATCGTCTAGGCTCAAGACAGTCTGGCCACACGAGGAGTACACCGATTGA  
 1401 GGGAGTACTTCAATGGAGGTTGCAGATCTCAACTCACCCCTAAAGATTGCAGGAGCATTTGGCTTTAAGGA  
 1471 CATAAATCCGAGCCATTGGAAGATTGCGGTGCCAGTGGTATCCACACTCTTCCCTCCAGCTGCACCCCTA  
 1541 GCACATGCAATCGGAGAAGGTGTAGACTACCTCTGGCGGACGAGGCCCAAGCAGCTCAGGGACAGCTC  
 1611 GAGCCGCGTCAGGAAAAGCTAGAGCTGCTCAGGACGAATAAGGCAGCTAAGCTCGCAGCTGACAAGGG  
 1681 GTGCGAGGTAGTCGCCAACAATGTTCCAGGTGCCCAAGATCCCATTTGTTGATGGCATTTCTGGCATCCCCA  
 1751 GGAATCCTGCGTGGCGCACACAACCTCGACTGCGTGCTATGGGAGGGAGGCCACTCTTTTCCCTGTTGTCA

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1821 TTACGACACTCGAGGATGAGCTGACCCCCAAGGCACCTGAACAGCAAAATGTTGCTGTCAATTGAAGGTGT  
 1891 GCGAGAGGACCTCCAGCCTCCATCCCAACGGGGATCCTTCAATTCGAACTCTCTCTGGCCATAGAGTCTAT  
 1961 GGCTATGCCCCAGACGGAGTACTGCCCTCTGGAGACCGGGAGAGACTACACCGTTGTCCCAATTGATGATG  
 2031 TGTGGACGATAGCATAAATGCTGTCGAGGACCCCATACCTCCAATCATAGGGAACAGCGGCAACCTAGC  
 2101 CATAGCATACATGGATGCTTTCAGGCCCAAGGTCCCCATCCACGTGGCTATGACAGGGGCCCTCAATGCC  
 2171 CGCGGTGAGATCGAGAGTGTACGTTCCGVAGCACCAAACTCGCCACAGCCACCGACTTGGCATGAAGT  
 2241 TAGCTGGTCTGGAGCCTATGACATTAATACAGGACCTAACTGGCAACGTTTCGTCAAACGTTTCCCTCA  
 2311 CAATCCCCGAGACTGGGACAGGTGGCCTACCTCAACCTTCTTATCTCCACCAACAGCAGGACGTCAG  
 2381 TTCCATCTAGCCCTGGCTGCCCTCCGAGTTCAAAGAGACCCAGAACTCGAAGACGCTGTGCGGCAATGG  
 2451 ATGCCGCTGCAATGCCGACCCATTGTTCCGCTCAGCTCTCCAGGCTTTCATGTGGTTGGAAGAAAACGG  
 2521 GATTGTGACCGACATGGCTAACTTCGCCCTCAGCGACCCAAAGCGCATAGGATGAAAACCTTCTTAGCA  
 2591 AAGCACCCAGGCTGGAAGCAAGTCCGAGAGGGCCAAAGTATGGCACGGCAGGCTACGGAGTGGAGGCTC  
 2661 GAGCCCCACACACAGAAGAGGCACAGAGGAAAGACACACCGGATCTCCAAGAAGATGGAACAATGGG  
 2731 CATCTACTTCGGACACCGGAATGGGTGGCTCTCAACGGGCACCGAGGCCCAAGCCCGGCCAACTCAAG  
 2801 TACTGGCAAAACACAGAGAAATACAGAGCCCAATGAGGACTACCCAGACTATGTGCACGGGAGAGA  
 2871 GCCGGTTGGCTCAGAAGAACAGATCCTACGGGCAGCCACGTCGATCTACGGGGCTCCAGGACAGGCTGA  
 2941 ACCACCCAGGCCCTTCATAGACGAGGTGCCAGGGTCTATGAAATCAACCATGGCGTGGTCCAAACCCAG  
 3011 GAGCAGATGAAGGACCTGCTCCTGACTGCGATGGAGATGAAGCATCGCAATCCAGGGGGCTCCACCAA  
 3081 AGCCAAAGCCAAACCCCAATGCTCCATCACAGAGACCCCTGGACGGCTGGCCGCTGGATCAGGACGGT  
 3151 CTCGACGAGGACTTGGAGTGGGCTCCTGGGAGTCTCCCGACACTACCCGCGCAGGTGTGGACACCAAT  
 3221 TCGGCCCTTCTACCATCCCAATTGGATCCGTTCCGGGGTCCCCCT

Total number of bases is: 3264.

DNA sequence composition: 834 A; 942 C; 853 G; 635 T;

Sequence name: 23-82A (SEQ ID NOS: 31 and 33)

Fig.4B

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Fig.5A

1	GGATACGATCGGTCGTGACCCCGGGGAGTCACCCGGGGACAGGCCGTCAAGGCCITGTTCAGGATGGGA	10		20		30		40		50		60		70
71	CTCCTCCTTCTACAACGCTATCATTGATGGTTAGTAGAGATCAGACAAACGATCGACGGATGACAAACC													
141	TGCAAGATCAAAACCCAAACAGATTGTTCCGTTTCATACGGAGCCTTCTGATGCCAACAAACGGACCGCGTC													
211	CATTCCGGACGACACCCCTGGAGAACACACTCTCAGGTGAGAGACCTCGACCTACAATTTGACTGTGGGG													
281	GACACAGGTCAGGGCTAATTGTCCTTTTCCCTGGATCCCTGGCTCAATTTGTTGGTGTCACTACACAC													
351	TGCAGGGCAATGGGAACACAAAGTTCCGATCAGATGCTCTGACTGCCCAGAACCTACCGGCCAGTTACAA													
421	CTACTGCAGGCTAGTGAGTCGGAGTCTCACAGTGAGGTCAAGCACACTTCTTGGTGGCGTTTATGCACATA													
491	AACGGCACCATAAACGCCGTGACCTTCCAAGGAAGCCTGAGTGAACCTGACAGATGTTAGCTACAATGGGT													
561	TGATGTCGCAACAGCCCAACATCAACGACAAATTGGGAACGTCTAGTAGGGGAAGGGTCACCGTCCT													
631	CAGCTTACCCACATCATATGATCTTGGGTATGTGAGGCTTGGTGACCCCATTCGCCCAATAGGGCTTGAC													
701	CCAAATAATGGTAGCCACATGTGACAGCAGTGACAGGCCAGAGTCTACACCATAACTGCAGCCGATGATT													
771	ACCAATTCTCATCACAGTACCAACAGGTGGGTAAACAATCACACTGTTCTCAGCCAACATTTGATGCCAT													
841	CACAAGCCTCAGCGTTGGGGAGAGCTCGTGTTTCAACAAGCGTCCACGGCTTGACTGGCGCCACC													
911	ATCTACCTCATAGGCTTTGATGGGACAAACGGTAATCACAGGGCTGTGGCCGCAACAATGGGCTGACGA													
981	CCGGCACCGACAACCTTATGCCATTCAATCTTGTGATTCCAACAACGAGATAACCCAGCCAATCACATC													
1051	CATCAAACTGGAGATAGTGACCTCCAAAGTGGTGGTCAGGCAGGGATCAGATGTCATGGTCGGCAAGA													
1121	GGAGCCTAGCAGTGACGATCCATGGTGGCAACTATCCAGGGGCCCTCCGTCCCGTCACGCTAGTGGCCT													
1191	ACGAAAGAGTGGCAACAGGATCCGTGTTACGGTCGCTGGGGTGAGCAACTTCGAGCTGATCCCAAATCC													
1261	TGAACTAGCAAGAACCCTGGTTACAGAAACGGCCGATTTGACCCAGGAGCCATGAACACACAAAATTG													
1331	ATACTGAGTGAGAGGACCGTCTTGGCATCAAGACCGTCTGGCCAAACAGGGAGTACACTGACTTTCGTG													
1401	AATACTTCATGGAGGTGCCGACCTCAACTCTCCCTGAAGATTGCAGGAGCATTCGGCTTCAAAGACAT													
1471	AATCCGGGCCATAAGGAGGATAGCTGTGCCGGTGGTCTCCACATTGTTCCACCTGCCGTCCCTAGCC													
1541	CATGCAATTGGGGAAGGTGTAGACTACCTGCTGGCGATGAGGCACAGGCTGCTTCAGGAACTGCTCGAG													
1611	CCGCGTCAGGAAAGCAAGAGCTGCTCAGGCCGCTAAGGCAGCTGACTCTCGCCGCCGACAAGGGTA													
1681	CGAGGTAGTCGCGAATCTATTCCAGGTGCCCCAGAAATCCCGTAGTCGACGGGATTCTTGTTCACCTGGG													
1751	GTACTCCGGGTGCACACAACCTCGACTGCGTGTAAAGAGAGGGTGCCACGCTATTCCTGTGGTTATTA													

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1821 CGACAGTGAAGACGCCATGACACCCAAAGCATTTGAACAGCAAAATGTTGCTGTCATTGAAGGCGTGCG
1891 AGAAGACCTCCAACCTCCATCTCAAGAGGATCCTTTCATACGAACCTCTCTGACACAGAGTCTATGGA
1961 TATGCTCCAGATGGGTACTTCCACTGGAGACTGGAGAGACTACACCGTTGTCCCAATAGATGATGCT
2031 GGGACGACAGCATTATGCTGTCCAAAGATCCCATACCTCCTATTGTGGAAACAGTGGAAATCTAGCCAT
2101 AGCTTACATGGATGTGTTTCGACCCAAAGTCCCAATCCATGTTGGCTATGACGGGAGCCCTCAATGCTTGT
2171 GCGAGATTGAGAAAGTAAGCTTTAGAAGCACCAGCTCGCCACTGCACACCGACTTGGCCTTAGGTTGG
2241 CTGGTCCGGAGCATTCGATGTAAACACCGGCCCAACTGGGCAACGTTTCATCAACGTTTCCCTCACAA
2311 TCCACGCCACTGGGACAGGCTCCCCTACCTCAACCTACCATACCTTCCACCCAAATGCAGGACGCCAGTAC
2381 CACCTTGCCATGGCTGCATCAGAGTTCAAGAGACCCCCGAACCTCGAGAGTGCCGTGAGAGCAATGGAAG
2451 CAGCAGCCAAAGTGGACCCACTATTCCAATCTGCACTCAGTGTGTTTCATGTTGGCTGGAAGAGAAATGGGAT
2521 TGTGACTGACATGGCCAACTTCGCACTCAGGACCCGAAACGCCCATCGGATCGAAATTTTCTTGCAAAC
2591 GCACCACAAGCAGGACAGCAAGTCGCAAGGGCCCAAGTACGGGACAGCAGGCTACGGAGTGGAGGCTCGGG
2661 GCCCCACACGAGGAGACAGACAGAGGGAAGAACACACAGGATCTCAAGAAGATGGAGACCATGGGCAT
2731 CTACTTTGCAACACCAGAAATGGGTAGCACTCAATGGGCACCGAGGCCCCAGCCAGCTAAAGTAC
2801 TGGCAGAACACGAGAAATACCGGACCCCAACGAGGACTATCTAGACTACGTGCATGCAGAGAAGAGCC
2871 GGTGGCATCAGAAGAACAATCCTAAGGGCAGCTACGTGATCTACGGGGCTCCAGGACAGGCAGAGCC
2941 ACCCAAGCTTTCATAGACGAAGTTGCCAAAGTCTATGAAATCAACCATGGACGTGGCCCAACCAAGAA
3011 CAGATGAAAGATCTGCTCTTGACTGCGATGGAGATGAAGCATCGCAATCCCAGGGCGGCTCTACCAAAGC
3081 CCAAGCCAAACCCCAATGCTCCAACACAGAGACCCCTGGTCGGCTGGGCCGCTGGATCAGGACCGTCTC
3151 TGATGAGGACCTTGAGTGAGGCTCCTGGGAGTCTCCCGACACCAACCCGCGCAGGTGTGGACACCAATTCCG
3221 GCCTTACAACATCCCAAAATTGGATCCGTTGCGGGTCCCT

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Total number of bases is: 3261.

DNA sequence composition: 873 A; 909 C; 847 G; 632 T; 0 OTHER;

Sequence name: D78F (SEQ ID NOS: 27 and 29)

**Fig.5B**

Fig.6A

1	GGATACGATGGGCTCTGACCCCTCTGGGAGTCACGAATTAAACGTGGCTACTAGGGGCGGATACCCGCCGCTGG	10
71	CCGCCACGTTAGTGGCTCCTCTCTTGTGATGATTCGCCACCATTGAGTGACATTTTCAACAGTCCACAGGC	20
141	GCGAAGCACGATCTCAGCAGCGTTCCGCATAAAGCCTACTGCTGGACAAGACGTGGAAGAACTCTTGATC	30
211	CCTAAAGTTTGGGTGCCACCTGAGGATCCGCTTGCCAGCCCTAGTGCAGTGGCAAAGTTCCCTCAGAGAGA	40
281	ACGGCTACAAAGTTTIGCAGCCACGGTCTCTGCCCGAGAATGAGGAGTATGAGACCGACCAATACTCCC	50
351	AGACTTAGCATGGATGCGACAGATAGAAGGGCTGTTTTAAACCCACTCTATCTCTCCCTATTGGAGAT	60
421	CAGGAGTACTTCCCAAAGTACTACCCAAACACATCGCCCTAGCAAGGAGAAGCCCAATGCGTACCCGCCAG	70
491	ACATCGCACTACTCAAGCAGATGATTTACCTGTTTCTCCAGGTTCCAGAGGCCAACGAGGCTTAAAGGA	
561	TGAAGTAACCTCTTGACCCAAACATAAAGGACAAGGCCCTATGGAAGTGGGACCTACATGGGACAAGCA	
631	AATCGACTTGCGCCATGAAGGAGGTGCGCCACTGGAAGAAACCCAAACAAAGGATCCTCTAAAGCTTGGGT	
701	ACACTTTTGAGAGCATCGCGCAGCTACTTGACATCACACTACCGGTAGGCCACCCGGTGAGGATGACAA	
771	GCCCTGGG TGCCACTCACAAGAGTGCCGTACGGATGTTGGTGTGCTGACGGGAGACGTAGATGGGACTTT	
841	GAGGTTGA AGATTACCTTCCCAAATCAACCTCAAGTCAATCAAGTGGACTACCATATGTAGGTGCAACCA	
911	AAGGAGAGACAAATTGGCGAGATGATAGCTATCTCAACCCAGTTTCTCAGAGAGCTATCAACACTGTTGAA	
981	GCAAGGTGCAGGGACAAAGGGGTCAAAACAAGAAGAGCTACTCAGCATGTTAAGTGACTATTGGTACTTA	
1051	TCAT GCGGGCTTTTGTTCCAAAGGCTGAAGGTACGACAAAGTACATGGCTCACCAAGACCCGGAACA	
1121	TATGGTCAGCTCCATCCCCAACACACCTCATGATCTCTATGATCACCTGGCCCGTGTGTCCAAACAGCCC	
1191	AAAT AACGTGTTGAACATTGAAGGGTGTCCTACTCTACAAATTCAACCCGTTTCAAGGAGGGTTGAAC	
1261	AGGA TCGTCGAGTGGATATTGGCCCGGAAGAACCCCAAGGCTCTTGATATGCGGACAAACATATACATTG	
1331	TCCA CTCAAACACGTGGTACTCAATTGACCTAGAGAAGGTGAGGCAAACTGCACCTCGCCAACACATGCA	
1401	AGCCGCAATGTACTACATACTCACCAGAGGGTGGTCAGACACACGGGACCCCAATGTTCAATCAAAACATGG	
1471	GCCACCTTTGCCATGAACATTGCCCTTGCTCTAGTGGTGGACTCATCGTGCCTGATAATGAACCTGCAAA	
1541	TTAAGACCTATGGTCAAGGCAGCGGGAAATGCAGCCACGTTTCATCAACAACCACTCTTTGAGCACACTAGT	
1611	GCTTGACCAGTGAACCTGATGAGACAGCCAGACGAGGAGTTCAAATCAAATTGAGGACAAG	
1681	CTAGGTATCAACTTTAAGATTGAGAGGTCCTATTGATGATATCAGGGGCAAGCTGAGACAGCTTGTCTCC	
1751	TTGCACAACCAAGGTTACCTGAGTGGGGGGTTGAACCAGAAACAATCCAGGCCCAACTGTTGAGCTTGACCT	



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1821 ACTAGGGTGGTCAGCTACATACAGCAAGAATCTCGGGATCTATGTGCCGGTGCTTGACAAGGAACGGCCTA
1891 TTTTGTCTGCTGCGTATCCCAAGGGAGTAGAGAACAGAGTCTCAAGTCCAAAGTCGGGATCGAGCAGG
1961 CATACAAGGTAGTCAGGTATGAGCGTTGAGGTGGTAGGTGGTTGGAACCTACCCACTCCTGAACAAAGC
2031 CTGCAAGAATAACGCAGGCGCGCTCGGCGGCATCTGGAGGCCAAGGGTTCCCACTCGACGAGTTCCCTA
2101 GCCGAGTGGTCTGAGCTGTCAGAGTTCGGTGAGGCCTTCAAGGCTTCAATATCAAGCTGACCGTAACAT
2171 CTGAGAGCCTAGCCGAACCTGAACAAGCCAGTACCCCCAAGCCCCCAATGTCAACAGACCAGTCAACAC
2241 TGGGGACTCAAGGCAGTCAGCAACGCCCTCAAGACCGGTGCGTACAGGAACGAAGCCGGACTGAGTGGT
2311 CTGTCCTTCTAGCCACAGCAAGAAGCCGTCTGCAAGATGCAGTTAAGGCCAAGGCAGAGCCGAGAAAC
2381 TCCACAAGTCCAAGCCAGACGACCCCGATGCAGACTGGTTCGAAAGATCAGAACTCTGTGACACCTTCT
2451 GGAGAAAGCCGACATCGCCAGCAAGGTGCGCCACTCAGCACTCGTGGAAACAAGCGACGCCCTTGAAGCA
2521 GTTCAGTCGACTTCGGTGTACACCCCAAGTACCCAGAGTCAAGAACCCACAGACCGCCTCCAACCCCG
2591 TTGTTGGGCTCCACCTGCCGCCAAGAGAGCCACCGGTGTCCAGGCCGCTCTTCTCGGAGCAGGAACGAG
2661 CAGACCAATGGGGATGGAGGCCCAACACGGTCCAAGAACGCCGTGAAATGGCCAAACGGGGCAACGC
2731 CAAAGGAGAGCCGCTAACAGCCATGATGGGAACCACTCAAGAAGAGGACACTAATCCCAGACCCCGTAT
2801 CCCCAGCCTTCGCCTGCGGGGGCCCCC

```

Total number of bases 1s: 2827.

DNA sequence composition: 796 A; 770 C; 724 G; 537 T; 0 OTHER;

Sequence name: P2B (SEQ ID No: 25)

Fig.6B

## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US97/12955**A. CLASSIFICATION OF SUBJECT MATTER**

IPC(6) : Please See Extra Sheet.

US CL : Please See Extra Sheet.

According to International Patent Classification (IPC) or to both national classification and IPC

**B. FIELDS SEARCHED**

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 424/184.1, 204.1, 816, 826; 435/71.1, 235.1, 236, 237, 238, 239, 320.1; 536/23.72

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, STN-MEDLINE, BIOSIS, CAPLUS, CABA

**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	MUNDT et al. Complete Nucleotide Sequences of 5'- and 3' Noncoding Regions of Both Genome Segments of Different Strains of Infectious Bursal Disease Virus. Virology. 1995, Vol. 209, pages 10-18, see entire document.	1-2, 4-20
X	US 4,530,831 A (LUTTICKEN ET AL) 23 JULY 1985 (07/23/85), see entire document.	7, 15-20
X	US 5,192,539 A (VAN DER MAREL ET AL) 09 MARCH 1993 (09/03/93), see entire document.	1-3, 7, 15-20
X	MUNDT et al. Identification of a novel viral protein in infectious bursal disease virus-infected cells. Journal of General Virology. 1995, Vol. 76, pages 437-443, see entire document.	8



Further documents are listed in the continuation of Box C.



See patent family annex.

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*O* document referring to an oral disclosure, use, exhibition or other means	
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Date of the actual completion of the international search

22 SEPTEMBER 1997

Date of mailing of the international search report

10 NOV 1997

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DATQUAN LEE

Telephone No. (703) 308-0196

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US97/12955

## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	BAYLISS et al. A comparison of the sequences of segment A of four infectious bursal disease virus strain and identification of a variable region in VP2. Journal of General Virology. 1990, Vol. 71, pages 1303-1312, see entire document.	1-2, 5-8, 10-13
Y	MORGAN et al. Sequence of the Small Double-Stranded RNA Genomic Segment of Infectious Bursal Disease Virus and Its Deduced 90kDa Product. Virology. 1988, Vol. 163, pages 240-242, see entire document.	1-20
Y	SPIES et al. Nucleotide sequence of infectious bursal disease virus genome segment A delineates two major open reading frames. Nucleic Acids Research. 1989, Vol. 17, No. 19, page 7982, see entire document.	1-20
Y	WO 91/16925 A1 (UNIVERSITY OF MARYLAND at COLLEGE PARK) 14 NOVEMBER 1991 (14/11/91), see entire document.	1-20

**INTERNATIONAL SEARCH REPORT**

International application No.

PCT/US97/12955

**A. CLASSIFICATION OF SUBJECT MATTER:**

IPC (6):

A61K 39/00, 39/38, 39/12; C12P 21/04; C12N 7/00, 7/01, 7/02, 7/04, 7/06, 7/08, 15/00, 15/09, 15/63, 15/70, 15/74

**A. CLASSIFICATION OF SUBJECT MATTER:**

US CL :

424/184.1, 204.1, 816, 826; 435/71.1, 235.1, 236, 237, 238, 239, 320.1; 536/23.72

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